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SEQUENCE LISTING

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<120> GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR

<130> A-401D

<140> 08/866,354
<141> 1997-05-30

<150> US 60/015,907
<151> 1996-04-22

<150> US 60/017,221
<151> 1996-05-09

<150> US 08/837,199
<151> 1997-04-14

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<170> PatentIn version 3.2

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<222> (2256)..(2294)
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between different receptor clones

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ccggcggcgg tggtgctgc cagaccggga gtttctctt tcaactggatg gagctgaact	420
ttgggcggcc agagcagcac agctgtccgg ggatcgctgc acgctgagct ccctcggcaa	480
gaccagcgg cggtcggga tttttttggg ggggcgggga ccagccccgc gccggcacc	539
atg ttc ctg gcg acc ctg tac ttc gcg ctg ccg ctc ttg gac ttg ctc	587
Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu	
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ctg tcg gcc gaa gtg agc ggc gga gac cgc ctg gat tgc gtg aaa gcc	635
Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala	
20 25 30	
agt gat cag tgc ctg aag gag cag agc tgc agc acc aag tac cgc acg	683
Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr	
35 40 45	
cta agg cag tgc gtg gcg ggc aag gag acc aac ttc agc ctg gca tcc	731
Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser	
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ggc ctg gag gcc aag gat gag tgc cgc agc gcc atg gag gcc ctg aag	779
Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys	
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cag aag tcg ctc tac aac tgc cgc tgc aag cgg ggt atg aag aag gag	827
Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu	
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aag aac tgc ctg cgc att tac tgg agc atg tac cag agc ctg cag gga	875
Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly	
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Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu	
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Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln	
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gtg gag cac att ccc aaa ggg aac aac tgc ctg gat gca gcg aag gcc	1019
Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala	
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Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr	
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Pro Cys Thr Thr 180 Ser Val Ser Asn Asp 185 Val Cys Asn Arg Arg 190 Lys Cys	
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His Lys Ala Leu Arg Gln Phe Phe 200 Asp Lys Val Pro Ala Lys His Ser 205	
tac gga atg ctc ttc tgc tcc tgc cgg gac atc gcc tgc aca gag cgg	1211
Tyr Gly Met Leu Phe Cys Ser 215 Cys Arg Asp Ile Ala Cys Thr Glu Arg 220	
agg cga cag acc atc gtg cct gtg tgc tcc tat gaa gag agg gag aag	1259
Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr 235 Glu Glu Arg Glu Lys 240 225	
ccc aac tgt ttg aat ttg cag gac tcc tgc aag acg aat tac atc tgc	1307
Pro Asn Cys Leu Asn Leu Gln Asp Ser 250 Cys Lys Thr Asn Tyr Ile Cys 255 245	
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Arg Ser Arg Leu Ala Asp Phe Phe 265 Thr Asn Cys Gln Pro Glu Ser Arg 270 260	
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Ser Val Ser 275 Ser Cys Leu Lys 280 Glu Asn Tyr Ala Asp Cys Leu Leu Ala 285	
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Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys 315 Ser Asn Ser Gly Asn 320 305 310	
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Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr 335 325 330	
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Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr 350 340 345	
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Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr 365 355 360	
act gcc ctc cgg gtt aag aac aag ccc ctg ggg cca gca ggg tct gag	1691
Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro 380 Ala Gly Ser Glu 370 375	
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Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser 415 405 410	
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Asn Gly Asn Tyr 420 Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr 430 425 430	

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Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu
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gtc ctg gtg gta acc gct ctg tcc acc cta tta tct tta aca gaa aca 1931
Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr
450 455 460

tca tagctgcatt aaaaaaatac aatatggaca tgtaaaaaga caaaaaccaa 1984
Ser
465

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Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
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Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
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Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
85 90 95

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Ser	Asp	Ile	Phe	Arg	Val	Val	Pro	Phe	Ile	Ser	Asp	Val	Phe	Gln	Gln
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Val	Glu	His	Ile	Pro	Lys	Gly	Asn	Asn	Cys	Leu	Asp	Ala	Ala	Lys	Ala
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Cys	Asn	Leu	Asp	Asp	Ile	Cys	Lys	Lys	Tyr	Arg	Ser	Ala	Tyr	Ile	Thr
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Pro	Cys	Thr	Thr	Ser	Val	Ser	Asn	Asp	Val	Cys	Asn	Arg	Arg	Lys	Cys
			180					185					190		
His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser
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Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg
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Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Lys
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Pro	Asn	Cys	Leu	Asn	Leu	Gln	Asp	Ser	Cys	Lys	Thr	Asn	Tyr	Ile	Cys
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Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	Ser	Arg
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Ser	Val	Ser	Ser	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala
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Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Ile	Asp	Ser
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Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn
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Asp	Leu	Glu	Glu	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr
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Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	Val	Thr
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Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
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Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
370 375 380

Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
385 390 395 400

Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser
405 410 415

Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr
420 425 430

Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu
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Ser
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gaactttgag tggccagagg agcgcagtcg cccggggatc gctgcacgct gagctctctc 240
cccagaccg ggcggcggct ttggattttg ggggggaggg gaccagctgc gcggcggcac 300
c atg ttc cta gcc act ctg tac ttc gcg ctg cca ctc ctg gat ttg ctg 349
Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
1 5 10 15
atg tcc gcc gag gtg agt ggt gga gac cgt ctg gac tgt gtg aaa gcc 397
Met Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
20 25 30

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Ser	Asp	Gln	Cys	Leu	Lys	Glu	Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	Thr	
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cta	agg	cag	tgc	gtg	gcg	ggc	aag	gaa	acc	aac	ttc	agc	ctg	aca	tcc	493
Leu	Arg	Gln	Cys	Val	Ala	Gly	Lys	Glu	Thr	Asn	Phe	Ser	Leu	Thr	Ser	
	50					55					60					
ggc	ctt	gag	gcc	aag	gat	gag	tgc	cgt	agc	gcc	atg	gag	gcc	ttg	aag	541
Gly	Leu	Glu	Ala	Lys	Asp	Glu	Cys	Arg	Ser	Ala	Met	Glu	Ala	Leu	Lys	
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cag	aag	tct	ctg	tac	aac	tgc	cgc	tgc	aag	cgg	ggc	atg	aag	aaa	gag	589
Gln	Lys	Ser	Leu	Tyr	Asn	Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu	
				85					90					95		
aag	aat	tgt	ctg	cgt	atc	tac	tgg	agc	atg	tac	cag	agc	ctg	cag	gga	637
Lys	Asn	Cys	Leu	Arg	Ile	Tyr	Trp	Ser	Met	Tyr	Gln	Ser	Leu	Gln	Gly	
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Asn	Asp	Leu	Leu	Glu	Asp	Ser	Pro	Tyr	Glu	Pro	Val	Asn	Ser	Arg	Leu	
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tca	gat	ata	ttc	cgg	gca	gtc	ccg	ttc	ata	tca	gat	gtt	ttc	cag	caa	733
Ser	Asp	Ile	Phe	Arg	Ala	Val	Pro	Phe	Ile	Ser	Asp	Val	Phe	Gln	Gln	
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gtg	gaa	cac	att	tcc	aaa	ggg	aac	aac	tgc	ctg	gac	gca	gcc	aag	gcc	781
Val	Glu	His	Ile	Ser	Lys	Gly	Asn	Asn	Cys	Leu	Asp	Ala	Ala	Lys	Ala	
145					150					155					160	
tgc	aac	ctg	gac	gac	acc	tgt	aag	aag	tac	agg	tcg	gcc	tac	atc	acc	829
Cys	Asn	Leu	Asp	Asp	Thr	Cys	Lys	Lys	Tyr	Arg	Ser	Ala	Tyr	Ile	Thr	
				165					170					175		
ccc	tgc	acc	acc	agc	atg	tcc	aac	gag	gtc	tgc	aac	cgc	cgt	aag	tgc	877
Pro	Cys	Thr	Thr	Ser	Met	Ser	Asn	Glu	Val	Cys	Asn	Arg	Arg	Lys	Cys	
			180					185					190			
cac	aag	gcc	ctc	agg	cag	ttc	ttc	gac	aag	gtt	ccg	gcc	aag	cac	agc	925
His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser	
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Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg	
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cgg	cga	cag	act	atc	gtc	ccc	gtg	tgc	tcc	tat	gaa	gaa	cga	gag	agg	1021
Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Arg	
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ccc	aac	tgc	ctg	agt	ctg	caa	gac	tcc	tgc	aag	acc	aat	tac	atc	tgc	1069
Pro	Asn	Cys	Leu	Ser	Leu	Gln	Asp	Ser	Cys	Lys	Thr	Asn	Tyr	Ile	Cys	
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aga	tct	cgc	ctt	gca	gat	ttt	ttt	acc	aac	tgc	cag	cca	gag	tca	agg	1117
Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	Ser	Arg	
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Ser	Val	Ser	Asn	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala	
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Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn	
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gac	ctg	gaa	gac	tgc	ttg	aaa	ttt	ctg	aat	ttt	ttt	aag	gac	aat	act	1309
Asp	Leu	Glu	Asp	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr	
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tgt	ctc	aaa	aat	gca	att	caa	gcc	ttt	ggc	aat	ggc	tca	gat	gtg	acc	1357
Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	Val	Thr	
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act	gcc	ttc	cgg	gtc	aag	aac	aag	cct	ctg	ggg	cca	gca	ggg	tct	gag	1453
Thr	Ala	Phe	Arg	Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	Glu	
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aat	gag	atc	ccc	aca	cac	gtt	tta	cca	ccc	tgt	gcg	aat	ttg	cag	gct	1501
Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	Gln	Ala	
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cag	aag	ctg	aaa	tcc	aat	gtg	tcg	ggg	agc	aca	cac	ctc	tgt	ctt	tct	1549
Gln	Lys	Leu	Lys	Ser	Asn	Val	Ser	Gly	Ser	Thr	His	Leu	Cys	Leu	Ser	
				405					410					415		
gat	agt	gat	ttc	gga	aag	gat	ggg	ctc	gct	ggg	gcc	tcc	agc	cac	ata	1597
Asp	Ser	Asp	Phe	Gly	Lys	Asp	Gly	Leu	Ala	Gly	Ala	Ser	Ser	His	Ile	
			420				425						430			
acc	aca	aaa	tca	atg	gct	gct	cct	ccc	agc	tgc	agt	ctg	agc	tca	ctg	1645
Thr	Thr	Lys	Ser	Met	Ala	Ala	Pro	Pro	Ser	Cys	Ser	Leu	Ser	Ser	Leu	
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Pro	Val	Leu	Met	Leu	Thr	Ala	Leu	Ala	Ala	Leu	Leu	Ser	Val	Ser	Leu	
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Ala	Glu	Thr	Ser													
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35 40 45

Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Thr Ser
50 55 60

Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
65 70 75 80

Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
85 90 95

Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
100 105 110

Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
115 120 125

Ser Asp Ile Phe Arg Ala Val Pro Phe Ile Ser Asp Val Phe Gln Gln
130 135 140

Val Glu His Ile Ser Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
145 150 155 160

Cys Asn Leu Asp Asp Thr Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
165 170 175

Pro Cys Thr Thr Ser Met Ser Asn Glu Val Cys Asn Arg Arg Lys Cys
180 185 190

His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
195 200 205

Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
210 215 220

Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Arg
225 230 235 240

Pro Asn Cys Leu Ser Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
245 250 255

Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
260 265 270

Ser Val Ser Asn Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
275 280 285

Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Val Asp Ser
290 295 300

Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
305 310 315 320

Asp Leu Glu Asp Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
325 330 335

Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
340 345 350

Met Trp Gln Pro Ala Pro Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
355 360 365

Thr Ala Phe Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
370 375 380

Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
385 390 395 400

Gln Lys Leu Lys Ser Asn Val Ser Gly Ser Thr His Leu Cys Leu Ser
405 410 415

Asp Ser Asp Phe Gly Lys Asp Gly Leu Ala Gly Ala Ser Ser His Ile
420 425 430

Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Ser Leu Ser Ser Leu
435 440 445

Pro Val Leu Met Leu Thr Ala Leu Ala Ala Leu Leu Ser Val Ser Leu
450 455 460

Ala Glu Thr Ser
465

<210> 5
<211> 3209

<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(510)
<223> note="1 to 510 is -237 to 272 of Fig 5 Hsgr-21bf"

<220>
<221> misc_feature
<222> (1)..(539)
<223> note="1 to 539 is -237 to 301 of Fig 5 Gdnfr"

<220>
<221> CDS
<222> (540)..(1937)

<220>
<221> misc_feature
<222> (1091)..(1091)
<223> N in position 1091 indicates any nucleic acid

<220>
<221> misc_feature
<222> (2078)..(2078)
<223> N in position 2078 indicates a position of divergence between different receptor clones

<220>
<221> misc_feature
<222> (2256)..(2294)
<223> N in positions 2256 to 2294 indicates positions of divergence between different receptor clones

```
<400> 5
aatctggcct cggaacacgc cattctccgc gccgcttcca ataaccacta acatccctaa      60
cgagcatccg agccgagggc tctgctcgga aatcgctctg gcccaactcg gcccttcgag      120
ctctcgaaga ttaccgcac tatttttttt ttcttttttt tcttttccta gcgcagataa      180
agtgagcccg gaaaggggaag gagggggcgg ggacaccatt gccctgaaag aataaataag      240
taaataaaca aactggctcc tcgccgcagc tggacgcggt cggttgagtc caggttgggt      300
cggacctgaa cccctaaaag cggaaccgcc tcccgccctc gccatcccgg agctgagtcg      360
ccggcgggcg tggctgctgc cagaccggga gtttctcttt tcaactggatg gagctgaact      420
ttgggcggcc agagcagcac agctgtccgg ggatcgctgc acgctgagct ccctcggcaa      480
gaccacgagg cggtctggga tttttttggg ggggcgggga ccagccccgc gccggcacc      539
atg ttc ctg gcg acc ctg tac ttc gcg ctg ccg ctc ttg gac ttg ctc      587
Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
1          5          10          15

ctg tcg gcc gaa gtg agc ggc gga gac cgc ctg gat tgc gtg aaa gcc      635
Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
          20          25          30
```

agt Ser	gat Asp	cag Gln 35	tgc Cys	ctg Leu	aag Lys	gag Glu 40	cag Gln	agc Ser	tgc Cys	agc Ser	acc Thr 45	aag Lys	tac Tyr	cgc Arg	acg Thr	683
cta Leu	agg Arg 50	cag Gln	tgc Cys	gtg Val	gcg Ala	ggc Gly 55	aag Lys	gag Glu	acc Thr	aac Asn	ttc Phe 60	agc Ser	ctg Leu	gca Ala	tcc Ser	731
ggc Gly 65	ctg Leu	gag Glu	gcc Ala	aag Lys	gat Asp 70	gag Glu	tgc Cys	cgc Arg	agc Ser	gcc Ala 75	atg Met	gag Glu	gcc Ala	ctg Leu	aag Lys 80	779
cag Gln	aag Lys	tcg Ser	ctc Leu	tac Tyr 85	aac Asn	tgc Cys	cgc Arg	tgc Cys	aag Lys 90	cgg Arg	ggt Gly	atg Met	aag Lys 95	aag Lys	gag Glu	827
aag Lys	aac Asn	tgc Cys	ctg Leu 100	cgc Arg	att Ile	tac Tyr	tgg Trp	agc Ser 105	atg Met	tac Tyr	cag Gln	agc Ser	ctg Leu 110	cag Gln	gga Gly	875
aat Asn	gat Asp	ctg Leu 115	ctg Leu	gag Glu	gat Asp	tcc Ser	cca Pro 120	tat Tyr	gaa Glu	cca Pro	gtt Val 125	aac Asn	agc Ser	aga Arg	ttg Leu	923
tca Ser	gat Asp 130	ata Ile	ttc Phe	cgg Arg	gtg Val	gtc Val 135	cca Pro	ttc Phe	ata Ile	tca Ser	gat Asp 140	gtt Val	ttt Phe	cag Gln	caa Gln	971
gtg Val 145	gag Glu	cac His	att Ile	ccc Pro	aaa Lys 150	ggg Gly	aac Asn	aac Asn	tgc Cys	ctg Leu 155	gat Asp	gca Ala	gcg Ala	aag Lys	gcc Ala 160	1019
tgc Cys	aac Asn	ctc Leu	gac Asp	gac Asp	att Ile	tgc Cys	aag Lys	aag Lys	tac Tyr 170	agg Arg	tcg Ser	gcg Ala	tac Tyr	atc Ile 175	acc Thr	1067
ccg Pro	tgc Cys	acc Thr 180	acc Thr	agc Ser	gtg Val	tcc Ser	aan Xaa	gat Asp 185	gtc Val	tgc Cys	aac Asn	cgc Arg	cgc Arg	aag Lys	tgc Cys	1115
cac His	aag Lys	gcc Ala 195	ctc Leu	cgg Arg	cag Gln	ttc Phe	ttt Phe 200	gac Asp	aag Lys	gtc Val	ccg Pro	gcc Ala 205	aag Lys	cac His	agc Ser	1163
tac Tyr	gga Gly 210	atg Met	ctc Leu	ttc Phe	tgc Cys	tcc Ser	tgc Cys	cgg Arg	gac Asp	atc Ile	gcc Ala 220	tgc Cys	aca Thr	gag Glu	cgg Arg	1211
agg Arg 225	cga Arg	cag Gln	acc Thr	atc Ile	gtg Val 230	cct Pro	gtg Val	tgc Cys	tcc Ser	tat Tyr 235	gaa Glu	gag Glu	agg Arg	gag Glu	aag Lys 240	1259
ccc Pro	aac Asn	tgt Cys	ttg Leu	aat Asn 245	ttg Leu	cag Gln	gac Asp	tcc Ser	tgc Cys 250	aag Lys	acg Thr	aat Asn	tac Tyr 255	atc Ile	tgc Cys	1307
aga Arg	tct Ser	cgc Arg	ctt Leu 260	gcg Ala	gat Asp	ttt Phe	ttt Phe 265	acc Thr	aac Asn	tgc Cys	cag Gln	cca Pro	gag Glu 270	tca Ser	agg Arg	1355
tct Ser	gtc Val	agc Ser 275	agc Ser	tgt Cys	cta Leu	aag Lys	gaa Glu 280	aac Asn	tac Tyr	gct Ala	gac Asp	tgc Cys 285	ctc Leu	ctc Leu	gcc Ala	1403

gaaacagctg gtactgatgt tcacctttat atatgtacta gcattttcca cgctgatgtt 2527
tatgtactgt aaacagttct gcaactcttg acaaaagaaa aaacacctgt cacatccaaa 2587
tatagtatct gtcttttcgt caaaatagag agtggggaat gagtgtgccg attcaatacc 2647
tcaatccctg aacgacactc tctaatacct aagccttacc tgagtgagaa gccctttacc 2707
taacaaaagt ccaatatagc tgaaatgtcg ctctaatact ctttacacat atgaggttat 2767
atgtagaaaa aaattttact actaaatgat ttcaactatt ggctttctat attttgaaag 2827
taatgatatt gtctcatttt tttactgatg gtttaataca aaatacacag agcttggttc 2887
ccctcataag tagtgttcgc tctgatatga acttcacaaa tacagctcat caaaagcaga 2947
ctctgagaag cctcgtgctg tagcagaaaag ttctgcatca tgtgactgtg gacaggcagg 3007
aggaacaga acagacaagc attgtctttt gtcattgctc gaagtgaag cgtgcatacc 3067
tgtggaggga actggtggct gcttgtaa atgtctgcagc atctcttgac acacttgtea 3127
tgacacaatc cagtaccttg gttttcaggt tatctgacaa aggcagcttt gattgggaca 3187
tggaggcatg ggcaggccgg aa 3209

<210> 6
<211> 465
<212> PRT
<213> HUMAN

<220>
<221> misc_feature
<222> (184)..(184)
<223> The 'Xaa' at location 184 stands for Lys, or Asn.

<400> 6

Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
1 5 10 15

Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
20 25 30

Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
35 40 45

Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
50 55 60

Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
65 70 75 80

Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
85 90 95

Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
 100 105 110
 Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
 115 120 125
 Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
 130 135 140
 Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
 145 150 155 160
 Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
 165 170 175
 Pro Cys Thr Thr Ser Val Ser Xaa Asp Val Cys Asn Arg Arg Lys Cys
 180 185 190
 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
 195 200 205
 Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
 210 215 220
 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys
 225 230 235 240
 Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
 245 250 255
 Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
 260 265 270
 Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
 275 280 285
 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser
 290 295 300
 Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
 305 310 315 320
 Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
 325 330 335
 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
 340 345 350

Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
355 360 365

Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
370 375 380

Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
385 390 395 400

Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser
405 410 415

Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr
420 425 430

Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu
435 440 445

Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr
450 455 460

Ser
465

<210> 7
<211> 508
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(508)
<223> Note="1 to 508 is -235 to 272 of Figure 5 Hsgr-21af"

<400> 7
tctggcctcg gaacacgcca ttctccgcgc cgcttccaat aaccactaac atccctaacg 60
agcatccgag ccgagggctc tgctcggaaa tcgtcctggc ccaactcggc ctttcgagct 120
ctcgaagatt accgcatcta tttttttttt cttttttttt ttttcctagc gcagataaag 180
tgagcccgga aaggggaagga gggggcgggg acaccattgc cctgaaagaa taaataagta 240
aataaacaaa ctggctcctc gccgcagctg gacgcggctg gttgagtcca gggtgggtcg 300
gacctgaacc cctaaaagcg gaaccgcctc ccgccctcgc catcccggag ctgagtcgcc 360
ggcggcggtg gctgctgcca gaccgggagt ttctctttt actggatgga gctgaacttt 420
gggcggccag agcagcacag ctgtccgggg atcgtctgcac gctgagctcc ctcggaaga 480
cccagcggcg gctcgggatt tttttggg 508

<210> 8

<211> 510
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(510)
<223> Note="1 to 510 is -237 to 272 of Figure 5 Hsgr-21bf"

<400> 8
aatctggcct cggaacacgc cattctccgc gccgcttcca ataaccacta acatccctaa 60
cgagcatccg agccgagggc tctgctcgga aatcgtcctg gcccaactcg gcccttcgag 120
ctctcgaaga ttaccgcac tttttttttt ttcttttttt tcttttccta gcgcagataa 180
agtgagcccg gaaaggggaag gagggggcgg ggacaccatt gccctgaaag aataaataag 240
taaataaaca aactggctcc tcgccgcagc tggacgcggt cggttgagtc caggttgggt 300
cggacctgaa ccctaaaag cggaaccgcc tcccgcctc gccatcccgg agctgagtcg 360
ccggcggcgg tggctgctgc cagaccggga gtttcctctt tcaactggatg gagctgaact 420
ttgggcggcc agagcagcac agctgtccgg ggatcgctgc acgctgagct ccctcggcaa 480
gaccacgcgg cggctcggga tttttttggg 510

<210> 9
<211> 1927
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(537)
<223> Note= "1 to 537 is -235 to 301 of Figure 5 21acon"

<220>
<221> CDS
<222> (538)..(1926)

<220>
<221> misc_feature
<222> (550)..(550)
<223> N in position 550 indicates any nucleic acid

<400> 9
tctggcctcg gaacacgcca ttctccgcgc cgtttccaat aaccactaac atccctaacg 60
agcatccgag ccgagggctc tgctcgga aa tcgtcctggc ccaactcggc ctttcgagct 120
ctcgaagatt accgcatcta tttttttttt cttttttttt ttttcctagc gcagataaag 180
tgagcccgga aaggggaagga gggggcgggg acaccattgc cctgaaagaa taaataagta 240
aataa caaa ctggctcctc gccgcagctg gacgcggctg gttgagtcca ggttgggtcg 300
gacctgaacc cctaaaagcg gaaccgcctc ccgcctcgc catcccggag ctgagtcgcc 360
ggcggcgggtg gctgctgcca gaccggagt ttctctttt actggatgga gctgaacttt 420

gggcggccag agcagcacag ctgtccgggg atcgctgcac gctgagctcc ctcggcaaga	480
cccagcggcg gctcgggatt tttttggggg ggcggggacc agccccgcgc cggcacc	537
atg ttc ctg gcg ncc ctg tac ttc gcg ctg ccg ctc ttg gac ttg ctc Met Phe Leu Ala Xaa Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu 1 5 10 15	585
ctg tcg gcc gaa gtg agc ggc gga gac cgc ctg gat tgc gtg aaa gcc Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala 20 25 30	633
agt gat cag tgc ctg aag gag cag agc tgc agc acc aag tac cgc acg Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr 35 40 45	681
cta agg cag tgc gtg gcg ggc aag gag acc aac ttc agc ctg gca tcc Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser 50 55 60	729
ggc ctg gag gcc aag gat gag tgc cgc agc gcc atg gag gcc ctg aag Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys 65 70 75 80	777
cag aag tcg ctc tac aac tgc cgc tgc aag cgg ggt atg aag aag gag Gln Lys Ser Leu Tyr 85 Asn Cys Arg Cys Lys 90 Arg Gly Met Lys 95 Lys Glu	825
aag aac tgc ctg cgc att tac tgg agc atg tac cag agc ctg cag gga Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly 100 105 110	873
aat gat ctg ctg gag gat tcc cca tat gaa cca gtt aac agc aga ttg Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu 115 120 125	921
tca gat ata ttc cgg gtg gtc cca ttc ata tca gat gtt ttt cag caa Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln 130 135 140	969
gtg gag cac att ccc aaa ggg aac aac tgc ctg gat gca gcg aag gcc Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala 145 150 155 160	1017
tgc aac ctc gac gac att tgc aag aag tac agg tcg gcg tac atc acc Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr 165 170 175	1065
ccg tgc acc acc agc gtg tcc aac gat gtc tgc aac cgc cgc aag tgc Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys 180 185 190	1113
cac aag gcc ctc cgg cag ttc ttt gac aag gtc ccg gcc aag cac agc His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser 195 200 205	1161
tac gga atg ctc ttc tgc tcc tgc cgg gac atc gcc tgc aca gag cgg Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg 210 215 220	1209
agg cga cag acc atc gtg cct gtg tgc tcc tat gaa gag agg gag aag Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys 225 230 235 240	1257

ccc aac tgt ttg aat ttg cag gac tcc tgc aag acg aat tac atc tgc	1305
Pro Asn Cys Leu Asn 245 Leu Gln Asp Ser Cys 250 Lys Thr Asn Tyr Ile Cys 255	
aga tct cgc ctt gcg gat ttt ttt acc aac tgc cag cca gag tca agg	1353
Arg Ser Arg Leu 260 Ala Asp Phe Phe Thr 265 Asn Cys Gln Pro Glu 270 Ser Arg	
tct gtc agc agc tgt cta aag gaa aac tac gct gac tgc ctc ctc gcc	1401
Ser Val Ser Ser Cys Leu Lys Glu 280 Asn Tyr Ala Asp Cys 285 Leu Leu Ala	
tac tcg ggg ctt att ggc aca gtc atg acc ccc aac tac ata gac tcc	1449
Tyr Ser Gly Leu Ile Gly Thr 295 Val Met Thr Pro Asn Tyr Ile Asp Ser	
agt agc ctc agt gtg gcc cca tgg tgt gac tgc agc aac agt ggg aac	1497
Ser Ser Leu Ser Val 310 Ala Pro Trp Cys Asp Cys 315 Ser Asn Ser Gly Asn 320	
gac cta gaa gag tgc ttg aaa ttt ttg aat ttc ttc aag gac aat aca	1545
Asp Leu Glu Glu Cys 325 Leu Lys Phe Leu Asn 330 Phe Phe Lys Asp Asn Thr 335	
tgt ctt aaa aat gca att caa gcc ttt ggc aat ggc tcc gat gtg acc	1593
Cys Leu Lys Asn 340 Ala Ile Gln Ala Phe 345 Gly Asn Gly Ser Asp Val Thr 350	
gtg tgg cag cca gcc ttc cca gta cag acc acc act gcc act acc acc	1641
Val Trp Gln Pro Ala Phe Pro Val 360 Gln Thr Thr Thr Ala Thr Thr Thr 365	
act gcc ctc cgg gtt aag aac aag ccc ctg ggg cca gca ggg tct gag	1689
Thr Ala Leu Arg Val Lys Asn 375 Lys Pro Leu Gly Pro 380 Ala Gly Ser Glu	
aat gaa att ccc act cat gtt ttg cca ccg tgt gca aat tta cag gca	1737
Asn Glu Ile Pro Thr His 390 Val Leu Pro Pro Cys 395 Ala Asn Leu Gln Ala 400	
cag aag ctg aaa tcc aat gtg tcg ggc aat aca cac ctc tgt att tcc	1785
Gln Lys Leu Lys Ser Asn Val Ser Gly 410 Asn Thr His Leu Cys Ile Ser 415	
aat ggt aat tat gaa aaa gaa ggt ctc ggt gct tcc agc cac ata acc	1833
Asn Gly Asn Tyr 420 Glu Lys Glu Gly Leu 425 Gly Ala Ser Ser His Ile Thr 430	
aca aaa tca atg gct gct cct cca agc tgt ggt ctg agc cca ctg ctg	1881
Thr Lys Ser Met Ala Ala Pro 440 Ser Cys Gly Leu Ser Pro Leu Leu 445	
gtc ctg gtg gta acc gct ctg tcc acc cta tta tct tta aca gaa a	1927
Val Leu Val Val Thr Ala 455 Ser Thr Leu Leu Ser Leu Thr Glu 460	

<210> 10
 <211> 463
 <212> PRT
 <213> HUMAN

<220>

<221> misc_feature

<222> (5)..(5)

<223> The 'Xaa' at location 5 stands for Thr, Ala, Pro, or Ser.

<400> 10

Met Phe Leu Ala Xaa Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
1 5 10 15

Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
20 25 30

Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
35 40 45

Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
50 55 60

Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
65 70 75 80

Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
85 90 95

Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
100 105 110

Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
115 120 125

Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
130 135 140

Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
145 150 155 160

Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
165 170 175

Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys
180 185 190

His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
195 200 205

Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
210 215 220

Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys
225 230 235 240

Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
245 250 255

Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
260 265 270

Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
275 280 285

Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser
290 295 300

Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
305 310 315 320

Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
325 330 335

Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
340 345 350

Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
355 360 365

Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
370 375 380

Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
385 390 395 400

Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser
405 410 415

Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr
420 425 430

Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu
435 440 445

Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
450 455 460

<210> 11
<211> 1929
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(539)
<223> Note= "1 to 539 is -237 to 301 of Figure 5 21bcon"

<220>
<221> CDS
<222> (540)..(1928)

<400> 11
aatctggcct cggaacacgc cattctccgc gccgcttcca ataaccacta acatccctaa 60
cgagcatccg agccgagggc tctgctcgga aatcgtcctg gcccaactcg gcccttcgag 120
ctctcgaaga ttaccgcac tattttttttt ttctttttttt tcttttctta gcgcagataa 180
agtgagcccg gaaaggggaag gagggggcg ggacaccatt gccctgaaag aataaataag 240
taaataaaca aactggctcc tcgccgcagc tggacgcggt cggttgagtc caggttgggt 300
cggacctgaa cccctaaaag cggaaccgcc tccgcacctc gccatcccg agctgagtcg 360
ccggcggcgg tggctgctgc cagaccgcga gtttctcttt tcaactggatg gagctgaact 420
ttgggcggcc agagcagcac agctgtcccg ggatcgctgc acgctgagct ccctcggcaa 480
gaccagcgg cggtcggga tttttttggg ggggcgggga ccagccccgc gccggcacc 539
atg ttc ctg gcg acc ctg tac ttc gcg ctg ccg ctc ttg gac ttg ctc 587
Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
1 5 10 15
ctg tcg gcc gaa gtg agc ggc gga gac cgc ctg gat tgc gtg aaa gcc 635
Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
20 25 30
agt gat cag tgc ctg aag gag cag agc tgc agc acc aag tac cgc acg 683
Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
35 40 45
cta agg cag tgc gtg gcg ggc aag gag acc aac ttc agc ctg gca tcc 731
Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
50 55 60
ggc ctg gag gcc aag gat gag tgc cgc agc gcc atg gag gcc ctg aag 779
Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
65 70 75 80
cag aag tcg ctc tac aac tgc cgc tgc aag cgg ggt atg aag aag gag 827
Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
85 90 95
aag aac tgc ctg cgc att tac tgg agc atg tac cag agc ctg cag gga 875
Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
100 105 110
aat gat ctg ctg gag gat tcc cca tat gaa cca gtt aac agc aga ttg 923
Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
115 120 125
tca gat ata ttc cgg gtg gtc cca ttc ata tca gat gtt ttt cag caa 971
Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
130 135 140

gtg	gag	cac	att	ccc	aaa	ggg	aac	aac	tgc	ctg	gat	gca	gcg	aag	gcc	1019
Val	Glu	His	Ile	Pro	Lys	Gly	Asn	Asn	Cys	Leu	Asp	Ala	Ala	Lys	Ala	
145					150					155					160	
tgc	aac	ctc	gac	gac	att	tgc	aag	aag	tac	agg	tgc	gcg	tac	atc	acc	1067
Cys	Asn	Leu	Asp	Asp	Ile	Cys	Lys	Lys	Tyr	Arg	Ser	Ala	Tyr	Ile	Thr	
				165					170					175		
ccg	tgc	acc	acc	agc	gtg	tcc	aac	gat	gtc	tgc	aac	cgc	cgc	aag	tgc	1115
Pro	Cys	Thr	Thr	Ser	Val	Ser	Asn	Asp	Val	Cys	Asn	Arg	Arg	Lys	Cys	
			180					185					190			
cac	aag	gcc	ctc	cgg	cag	ttc	ttt	gac	aag	gtc	ccg	gcc	aag	cac	agc	1163
His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser	
		195					200					205				
tac	gga	atg	ctc	ttc	tgc	tcc	tgc	cgg	gac	atc	gcc	tgc	aca	gag	cgg	1211
Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg	
	210					215					220					
agg	cga	cag	acc	atc	gtg	cct	gtg	tgc	tcc	tat	gaa	gag	agg	gag	aag	1259
Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Lys	
225					230					235					240	
ccc	aac	tgt	ttg	aat	ttg	cag	gac	tcc	tgc	aag	acg	aat	tac	atc	tgc	1307
Pro	Asn	Cys	Leu	Asn	Leu	Gln	Asp	Ser	Cys	Lys	Thr	Asn	Tyr	Ile	Cys	
				245				250						255		
aga	tct	cg	ctt	gcg	gat	ttt	ttt	acc	aac	tgc	cag	cca	gag	tca	agg	1355
Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	Ser	Arg	
			260					265					270			
tct	gtc	agc	agc	tgt	cta	aag	gaa	aac	tac	gct	gac	tgc	ctc	ctc	gcc	1403
Ser	Val	Ser	Ser	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala	
		275					280					285				
tac	tgc	ggg	ctt	att	ggc	aca	gtc	atg	acc	ccc	aac	tac	ata	gac	tcc	1451
Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Ile	Asp	Ser	
	290					295					300					
agt	agc	ctc	agt	gtg	gcc	cca	tgg	tgt	gac	tgc	agc	aac	agt	ggg	aac	1499
Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn	
305					310					315					320	
gac	cta	gaa	gag	tgc	ttg	aaa	ttt	ttg	aat	ttc	ttc	aag	gac	aat	aca	1547
Asp	Leu	Glu	Glu	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr	
				325					330					335		
tgt	ctt	aaa	aat	gca	att	caa	gcc	ttt	ggc	aat	ggc	tcc	gat	gtg	acc	1595
Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	Val	Thr	
			340					345					350			
gtg	tgg	cag	cca	gcc	ttc	cca	gta	cag	acc	acc	act	gcc	act	acc	acc	1643
Val	Trp	Gln	Pro	Ala	Phe	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr	
		355					360					365				
act	gcc	ctc	cgg	gtt	aag	aac	aag	ccc	ctg	ggg	cca	gca	ggg	tct	gag	1691
Thr	Ala	Leu	Arg	Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	Glu	
	370					375					380					
aat	gaa	att	ccc	act	cat	gtt	ttg	cca	ccg	tgt	gca	aat	tta	cag	gca	1739
Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	Gln	Ala	
385					390					395					400	

cag aag ctg aaa tcc aat gtg tgc ggc aat aca cac ctc tgt att tcc 1787
Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser
405 410 415

aat ggt aat tat gaa aaa gaa ggt ctc ggt gct tcc agc cac ata acc 1835
Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr
420 425 430

aca aaa tca atg gct gct cct cca agc tgt ggt ctg agc cca ctg ctg 1883
Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu
435 440 445

gtc ctg gtg gta acc gct ctg tcc acc cta tta tct tta aca gaa a 1929
Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
450 455 460

<210> 12
<211> 463
<212> PRT
<213> HUMAN

<400> 12

Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
1 5 10 15

Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
20 25 30

Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
35 40 45

Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
50 55 60

Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
65 70 75 80

Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
85 90 95

Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
100 105 110

Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
115 120 125

Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
130 135 140

Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
145 150 155 160

Cys	Asn	Leu	Asp	Asp	Ile	Cys	Lys	Lys	Tyr	Arg	Ser	Ala	Tyr	Ile	Thr	165	170	175
Pro	Cys	Thr	Thr	Ser	Val	Ser	Asn	Asp	Val	Cys	Asn	Arg	Arg	Lys	Cys	180	185	190
His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser	195	200	205
Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg	210	215	220
Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Lys	225	230	235
Pro	Asn	Cys	Leu	Asn	Leu	Gln	Asp	Ser	Cys	Lys	Thr	Asn	Tyr	Ile	Cys	245	250	255
Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	Ser	Arg	260	265	270
Ser	Val	Ser	Ser	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala	275	280	285
Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Ile	Asp	Ser	290	295	300
Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn	305	310	315
Asp	Leu	Glu	Glu	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr	325	330	335
Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	Val	Thr	340	345	350
Val	Trp	Gln	Pro	Ala	Phe	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr	355	360	365
Thr	Ala	Leu	Arg	Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	Glu	370	375	380
Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	Gln	Ala	385	390	395
Gln	Lys	Leu	Lys	Ser	Asn	Val	Ser	Gly	Asn	Thr	His	Leu	Cys	Ile	Ser	405	410	415

Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr
420 425 430

Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu
435 440 445

Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
450 455 460

<210> 13
<211> 699
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(699)
<223> Note= "1 to 699 is 814 to 1512 of Figure 5 Hsgr-29a"

<220>
<221> CDS
<222> (2)..(697)

<400> 13
g tcg gcg tac atc acc ccg tgc acc acc agc gtg tcc aat gat gtc tgc 49
Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys
1 5 10 15

aac cgc cgc aag tgc cac aag gcc ctc cgg cag ttc ttt gac aag gtc 97
Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val
20 25 30

ccg gcc aag cac agc tac gga atg ctc ttc tgc tcc tgc cgg gac atc 145
Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile
35 40 45

gcc tgc aca gag cgg agg cga cag acc atc gtg cct gtg tgc tcc tat 193
Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr
50 55 60

gaa gag agg gag aag ccc aac tgt ttg aat ttg cag gac tcc tgc aag 241
Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys
65 70 75 80

acg aat tac atc tgc aga tct cgc ctt gcg gat ttt ttt acc aac tgc 289
Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys
85 90 95

cag cca gag tca agg tct gtc agc agc tgt cta aag gaa aac tac gct 337
Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala
100 105 110

gac tgc ctc ctc gcc tac tcg ggg ctt att ggc aca gtc atg acc ccc 385
Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro
115 120 125

aac tac ata gac tcc agt agc ctc agt gtg gcc cca tgg tgt gac tgc 433
Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys
130 135 140

agc aac agt ggg aac gac cta gaa gag tgc ttg aaa ttt ttg aat ttc 481
Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe
145 150 155 160

ttc aag gac aat aca tgt ctt aaa aat gca att caa gcc ttt ggc aat 529
Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn
165 170 175

ggc tcc gat gtg acc gtg tgg cag cca gcc ttc cca gta cag acc acc 577
Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr
180 185 190

act gcc gct acc acc act gcc ctc cgg gtt aag aac aag ccc ctg ggg 625
Thr Ala Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly
195 200 205

cca gca ggg tct gag aat gaa att ccc act cat gtt ttg cca ccg tgt 673
Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys
210 215 220

gca aat tta cag gca cag aag ctg aa 699
Ala Asn Leu Gln Ala Gln Lys Leu
225 230

<210> 14
<211> 232
<212> PRT
<213> HUMAN

<400> 14

Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys
1 5 10 15

Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val
20 25 30

Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile
35 40 45

Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr
50 55 60

Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys
65 70 75 80

Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys
85 90 95

Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala
100 105 110

Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro
115 120 125

Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys
130 135 140

Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe
145 150 155 160

Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn
165 170 175

Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr
180 185 190

Thr Ala Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly
195 200 205

Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys
210 215 220

Ala Asn Leu Gln Ala Gln Lys Leu
225 230

<210> 15
<211> 2157
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(2157)
<223> Note= "1 to 2157 is 814 to 2971 of Figure 5 29brc"

<220>
<221> CDS
<222> (2)..(886)

<220>
<221> misc_feature
<222> (1204)..(1242)
<223> N in positions 1204 to 1242 indicates positions of divergence
between different receptor clones.

<400> 15
g tcg gcg tac atc acc ccg tgc acc acc agc gtg tcc aat gat gtc tgc 49
Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys
1 5 10 15

aac cgc cgc aag tgc cac aag gcc ctc ccg cag ttc ttt gac aag gtc 97
Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val
20 25 30

ccg gcc aag cac agc tac gga atg ctc ttc tgc tcc tgc cgg gac atc 145
Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile
35 40 45

[illegible]

aaaaagacaa aaaccaagtt atctgtttcc tgttctcttg tatagctgaa attccagttt 976
aggagctcag ttgagaaaca gttccattca actggaacat tttttttttt ccttttaaga 1036
aagcttcttg tgatccttcg gggcttctgt gaaaaacctg atgcagtgtt ccatccaaac 1096
tcagaaggct ttgggatatg ctgtatttta aaggacagct ttgtaacttg ggctgtaaaag 1156
caaactgggg ctgtgttttc gatgatgatg atcatcatga tcatgatnnn nnnnnnnnnn 1216
nnnnnnnnnn nnnnnnnnnn nnnnnngatt ttaacagttt tacttctggc ctttcctagc 1276
tagagaagga gttaatatct ctaaggtaac tcccatatct cttttaatga cattgatttc 1336
taatgatata aatttcagcc tacattgatg ccaagctttt ttgccacaaa gaagattctt 1396
accaagagtg ggctttgttg aaacagctgg tactgatgtt cacctttata tatgtactag 1456
cattttccac gctgatgttt atgtactgta aacagttctg cactcttgta caaaagaaaa 1516
aacacctgtc acatccaaat atagtatctg tcttttcgtc aaaatagaga gtggggaatg 1576
agtgtgccga ttcaatacct caatccctga acgacactct cctaataccta agccttacct 1636
gagtgagaag ccctttacct aacaaaagtc caatatagct gaaatgtcgc tctaatactc 1696
tttacacata tgagggtata tgtagaaaaa aattttacta ctaaagtatt tcaactattg 1756
gctttctata ttttgaaagt aatgatattg tctcattttt ttactgatgg tttaatacaa 1816
aatacacaga gcttggtttc cctcataagt agtggtcgtc ctgatatgaa cttcacaaat 1876
acagctcatc aaaagcagac tctgagaagc ctggtgctgt agcagaaagt tctgcatcat 1936
gtgactgtgg acaggcagga ggaaacagaa cagacaagca ttgtcttttg tcattgctcg 1996
aagtgcaagc gtgcatacct gtggagggaa ctggtggctg cttgtaaatg ttctgcagca 2056
tctcttgaca cacttgatcat gacacaatcc agtaccttg ttttcagggt atctgacaaa 2116
ggcagctttg attgggacat ggaggcatgg gcaggccgga a 2157

<210> 16
<211> 294
<212> PRT
<213> HUMAN

<400> 16

Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys
1 5 10 15

Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val
20 25 30

Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile
35 40 45

Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr
50 55 60

Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys
65 70 75 80

Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys
85 90 95

Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala
100 105 110

Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro
115 120 125

Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys
130 135 140

Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe
145 150 155 160

Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn
165 170 175

Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr
180 185 190

Thr Ala Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly
195 200 205

Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys
210 215 220

Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr
225 230 235 240

His Leu Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala
245 250 255

Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly
260 265 270

Leu Ser Pro Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu
275 280 285

Ser Leu Thr Glu Thr Ser
290

<210> 17
<211> 659

<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(659)
<223> Note= "1 to 659 is 1033 to 1691 of Figure 5 Hsgr-21ar"

<220>
<221> CDS
<222> (2)..(658)

<400> 17

g aat ttg cag gac tcc tgc aag acg aat tac atc tgc aga tct cgc ctt	49
Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu	
1 5 10 15	
gcg gat ttt ttt acc aac tgc cag cca gag tca agg tct gtc agc agc	97
Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser	
20 25 30	
tgt cta aag gaa aac tac gct gac tgc ctc ctc gcc tac tcg ggg ctt	145
Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu	
35 40 45	
att ggc aca gtc atg acc ccc aac tac ata gac tcc agt agc ctc agt	193
Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser	
50 55 60	
gtg gcc cca tgg tgt gac tgc agc aac agt ggg aac gac cta gaa gag	241
Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu	
65 70 75 80	
tgc ttg aaa ttt ttg aat ttc ttc aag gac aat aca tgt ctt aaa aat	289
Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn	
85 90 95	
gca att caa gcc ttt ggc aat ggc tcc gat gtg acc gtg tgg cag cca	337
Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro	
100 105 110	
gcc ttc cca gta cag acc acc act gcc act acc acc act gcc ctc cgg	385
Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg	
115 120 125	
gtt aag aac aag ccc ctg ggg cca gca ggg tct gag aat gaa att ccc	433
Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro	
130 135 140	
act cat gtt ttg cca ccg tgt gca aat tta cag gca cag aag ctg aaa	481
Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys	
145 150 155 160	
tcc aat gtg tcg ggc aat aca cac ctc tgt att tcc aat ggt aat tat	529
Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr	
165 170 175	
gaa aaa gaa ggt ctc ggt gct tcc agc cac ata acc aca aaa tca atg	577
Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met	
180 185 190	

gct gct cct cca agc tgt ggt ctg agc cca ctg ctg gtc ctg gtg gta 625
Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val
195 200 205

acc gct ctg tcc acc cta tta tct tta aca gaa a 659
Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
210 215

<210> 18
<211> 219
<212> PRT
<213> HUMAN

<400> 18

Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu
1 5 10 15

Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser
20 25 30

Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu
35 40 45

Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser
50 55 60

Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu
65 70 75 80

Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn
85 90 95

Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro
100 105 110

Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg
115 120 125

Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro
130 135 140

Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys
145 150 155 160

Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr
165 170 175

Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met
180 185 190

Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val
195 200 205

Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
210 215

<210> 19
<211> 630
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(630)
<223> Note= "1 to 630 is 1062 to 1691 of Figure 5 Hsgr-21br"

<220>
<221> CDS
<222> (3)..(629)

<400> 19
ac atc tgc aga tct cgc ctt gcg gat ttt ttt acc aac tgc cag cca 47
Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro
1 5 10 15
gag tca agg tct gtc agc agc tgt cta aag gaa aac tac gct gac tgc 95
Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys
20 25 30
ctc ctc gcc tac tcg ggg ctt att ggc aca gtc atg acc ccc aac tac 143
Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr
35 40 45
ata gac tcc agt agc ctc agt gtg gcc cca tgg tgt gac tgc agc aac 191
Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn
50 55 60
agt ggg aac gac cta gaa gag tgc ttg aaa ttt ttg aat ttc ttc aag 239
Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys
65 70 75
gac aat aca tgt ctt aaa aat gca att caa gcc ttt ggc aat ggc tcc 287
Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser
80 85 90 95
gat gtg acc gtg tgg cag cca gcc ttc cca gta cag acc acc act gcc 335
Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala
100 105 110
act acc acc act gcc ctc cgg gtt aag aac aag ccc ctg ggg cca gca 383
Thr Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala
115 120 125
ggg tct gag aat gaa att ccc act cat gtt ttg cca ccg tgt gca aat 431
Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn
130 135 140
tta cag gca cag aag ctg aaa tcc aat gtg tcg ggc aat aca cac ctc 479
Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu
145 150 155

tgt	att	tcc	aat	ggg	aat	tat	gaa	aaa	gaa	ggg	ctc	ggg	gct	tcc	agc	527
Cys	Ile	Ser	Asn	Gly	Asn	Tyr	Glu	Lys	Glu	Gly	Leu	Gly	Ala	Ser	Ser	
160					165					170					175	

cac	ata	acc	aca	aaa	tca	atg	gct	gct	cct	cca	agc	tgt	ggg	ctg	agc	575
His	Ile	Thr	Thr	Lys	Ser	Met	Ala	Ala	Pro	Pro	Ser	Cys	Gly	Leu	Ser	
				180					185					190		

cca	ctg	ctg	gtc	ctg	gtg	gta	acc	gct	ctg	tcc	acc	cta	tta	tct	tta	623
Pro	Leu	Leu	Val	Leu	Val	Val	Thr	Ala	Leu	Ser	Thr	Leu	Leu	Ser	Leu	
			195					200					205			

aca	gaa	a														630
Thr	Glu															

<210> 20
 <211> 209
 <212> PRT
 <213> HUMAN

<400> 20

Ile	Cys	Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	
1				5					10					15		

Ser	Arg	Ser	Val	Ser	Ser	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	
			20					25					30			

Leu	Ala	Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Ile	
		35					40					45				

Asp	Ser	Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	
	50					55					60					

Gly	Asn	Asp	Leu	Glu	Glu	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	
65					70					75					80	

Asn	Thr	Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	
				85					90					95		

Val	Thr	Val	Trp	Gln	Pro	Ala	Phe	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	
			100					105						110		

Thr	Thr	Thr	Ala	Leu	Arg	Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	
		115					120					125				

Ser	Glu	Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	
	130					135					140					

Gln	Ala	Gln	Lys	Leu	Lys	Ser	Asn	Val	Ser	Gly	Asn	Thr	His	Leu	Cys	
145					150					155					160	

Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His
165 170 175

Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro
180 185 190

Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr
195 200 205

Glu

<210> 21
<211> 1075
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(1075)
<223> Note= "1 to 1075 is 1255 to 2330 of Figure 5 Hsgr-2"

<220>
<221> CDS
<222> (2)..(445)

<220>
<221> misc_feature
<222> (763)..(801)
<223> N in position 763 to 801 indicates positions of divergence
between different receptor clones.

<400> 21
t ggg aac gac cta gaa gag tgc ttg aaa ttt ttg aat ttc ttc aag gac 49
Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp
1 5 10 15
aat aca tgt ctt aaa aat gca att caa gcc ttt ggc aat ggc tcc gat 97
Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp
20 25 30
gtg acc gtg tgg cag cca gcc ttc cca gta cag acc acc act gcc act 145
Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr
35 40 45
acc acc act gcc ctc cgg gtt aag aac aag ccc ctg ggg cca gca ggg 193
Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly
50 55 60
tct gag aat gaa att ccc act cat gtt ttg cca ccg tgt gca aat tta 241
Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu
65 70 75 80
cag gca cag aag ctg aaa tcc aat gtg tgc ggc aat aca cac ctc tgt 289
Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys
85 90 95

```

att tcc aat ggt aat tat gaa aaa gaa ggt ctc ggt gct tcc agc cac      337
Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His
                  100                      105                      110

ata acc aca aaa tca atg gct gct cct cca agc tgt ggt ctg agc cca      385
Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro
                  115                      120                      125

ctg ctg gtc ctg gtg gta acc gct ctg tcc acc cta tta tct tta aca      433
Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr
                  130                      135                      140

gaa aca tca tag ctgcattaaa aaaatacaat atggacatgt aaaaagacaa      485
Glu Thr Ser
145

aaaccaagtt atctgtttcc tggtctcttg tatagctgaa attccagttt aggagctcag      545
ttgagaaaca gttccattca actggaacat tttttttttt cctttttaaga aagcttcttg      605
tgatccttcg gggcttctgt gaaaaacctg atgcagtgtc ccatccaaac tcagaaggct      665
ttgggatatg ctgtatttta aaggacagt ttgtaacttg ggctgtaaag caaactgggg      725
ctgtgttttc gatgatgatg atcatcatga tcatgatnnn nnnnnnnnnn nnnnnnnnnn      785
nnnnnnnnnn nnnnnngatt ttaacagttt tacttctggc ctttcctagc tagagaagga      845
gttaatatatt ctaaggtaac tcccatatct cttttaatga cattgatttc taatgatata      905
aatttcagcc tacattgatg ccaagctttt ttgccacaaa gaagattctt accaagagtg      965
ggctttgtgg aaacagctgg tactgatgtt cacctttata tatgtactag cattttccac      1025
gctgatgttt atgtactgta aacagttctg cactcttgta caaaagaaaa      1075

<210> 22
<211> 147
<212> PRT
<213> HUMAN

<400> 22

Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp
1          5          10          15

Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp
                20          25          30

Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr
35          40          45

Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly
50          55          60

Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu
65          70          75          80

```

Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys
85 90 95

Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His
100 105 110

Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro
115 120 125

Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr
130 135 140

Glu Thr Ser
145

<210> 23
<211> 1059
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(1059)
<223> Note= "1 to 1059 is 1272 to 2330 of Figure 5 Hsgr-9"

<220>
<221> CDS
<222> (3)..(428)

<400> 23
ag tgc ttg aaa ttt ttg aat ttc ttc aag gac aat aca tgt ctt aaa 47
Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys
1 5 10 15

aat gca att caa gcc ttt ggc aat ggc tcc gat gtg acc gtg tgg cag 95
Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln
20 25 30

cca gcc ttc cca gta cag acc acc act gcc act acc acc act gcc ctc 143
Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu
35 40 45

cgg gtt aag aac aag ccc ctg ggg cca gca ggg tct gag aat gaa att 191
Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile
50 55 60

ccc act cat gtt ttg cca ccg tgt gca aat tta cag gca cag aag ctg 239
Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu
65 70 75

aaa tcc aat gtg tcg ggc aat aca cac ctc tgt att tcc aat ggt aat 287
Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn
80 85 90 95

tat gaa aaa gaa ggt ctc ggt gct tcc agc cac ata acc aca aaa tca 335
Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser
100 105 110

```

atg gct gct cct cca agc tgt ggt ctg agc cca ctg ctg gtc ctg gtg      383
Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val
              115                      120                      125

gta acc gct ctg tcc acc cta tta tct tta aca gaa aca tca tag      428
Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser
              130                      135                      140

ctgcattaaa aaaatacaat atggacatgt aaaaagacaa aaaccaagtt atctgtttcc      488

tggttctcttg tatagctgaa attccagttt aggagctcag ttgagaaaca gttccattca      548

actggaacat tttttttttt tccttttaag aaagcttctt gtgatccttt ggggcttctg      608

tgaaaaacct gatgcagtgc tccatccaaa ctgagaaggc tttgggatat gctgtatttt      668

aaagggacag tttgtaactt gggctgtaaa gcaaactggg gctgtgtttt cgatgatgat      728

gatgatcatg atgatgatca tcatgatcat gatgatgatc atcatgatca tgatgatgat      788

tttaacagtt ttacttctgg cttttcctag ctagagaagg agttaatatt tctaaggtaa      848

ctcccatatc tcctttaatg acattgattt ctaatgatat aaatttcagc ctacattgat      908

gccaagcttt tttgccacaa agaagattct taccaagagt gggctttgtg gaaacagctg      968

gtactgatgt tcacctttat atatgtacta gcattttcca cgctgatgtt tatgtactgt    1028

aaacagttct gcactcttgt acaaaagaaa a                                1059

```

```

<210>  24
<211> 141
<212>  PRT
<213>  HUMAN

```

<400> 24

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Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn
1              5              10              15

```

```

Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro
20              25              30

```

```

Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg
35              40              45

```

```

Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro
50              55              60

```

```

Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys
65              70              75              80

```

```

Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr
85              90              95

```

```

Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met
100              105              110

```

Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val
115 120 125

Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser
130 135 140

<210> 25
<211> 10
<212> PRT
<213> HUMAN

<400> 25

Gln Ser Cys Ser Thr Lys Tyr Arg Thr Leu
1 5 10

<210> 26
<211> 10
<212> PRT
<213> HUMAN

<400> 26

Cys Lys Arg Gly Met Lys Lys Glu Lys Asn
1 5 10

<210> 27
<211> 10
<212> PRT
<213> HUMAN

<400> 27

Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val
1 5 10

<210> 28
<211> 10
<212> PRT
<213> RAT

<400> 28

Cys Ser Tyr Glu Glu Arg Glu Arg Pro Asn
1 5 10

<210> 29
<211> 14
<212> PRT
<213> RAT

<400> 29

Pro Ala Pro Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr
1 5 10

<210> 30
<211> 21
<212> DNA
<213> HUMAN

<400> 30
ctgtttgaat ttgcaggact c 21

<210> 31
<211> 36
<212> DNA
<213> HUMAN

<400> 31
ctcctctcta agcttctaac cacagcttgg aggagc 36

<210> 32
<211> 37
<212> DNA
<213> HUMAN

<400> 32
ctcctctcta agcttctatg ggctcagacc acagctt 37

<210> 33
<211> 60
<212> DNA
<213> HUMAN

<400> 33
ctcctctcta agcttctact tgtcatcgtc gtccttgtag tcaccacagc ttggaggagc 60

<210> 34
<211> 60
<212> DNA
<213> HUMAN

<400> 34
ctcctctcta agcttctact tgtcatcgtc gtccttgtag tctggctcag accacagctt 60

<210> 35
<211> 4232
<212> DNA
<213> HUMAN

<220>
<221> CDS
<222> (1587)..(2978)

<400> 35
catgaagaaa cctcagtaag tctcagactt ggcccaaagg agcccaacta gttactccct 60
gggtctgttac agaggatctg gctattacac tcaacagcaa aaattcaatt caatcccgt 120
aaagatataa gaatcactag gaakaataag ccagaactca agacagaaat agcattaagt 180
agttccttca gtacagtgag cagaagctgg ccactctacg actctawaag actcagaaaa 240

gcttactagg gaccwctggg catwccggtg tcctatgtgg ggatttcgta acgtctttga	300
gtcagaagct gccctcaaaa tagtttcttc tcaaaacggt ttcaggcttt gttagaaagg	360
gaagacttca ctgccacttt acccagatca tctaccccat ccttggaatg aatggggaag	420
cttcagccac cctaccaggc tcctaaaatc accaacttga gagaaaaact ataacgttgc	480
tctaccagta cttcaggagg ttaaagaaag tcacagaaga aaagaactct ggggaaaaca	540
gtcaaattcg gctattaaga cattagttac aggccctgt acctctctc tagaaaccct	600
gggagtacac ccgcagagga gagagagccc aagccaccaa gcaaagtcaa ccaatctggc	660
aaaggggctg cccactgcgg ctttcagtcc aagaagtgga tcctgctggg tcgcagtctc	720
tcttctatct cctcacttcc tatttaccct ttgaagtggg tactgaatag cccgttccca	780
agcagaggcc ctttgtatac ggggtgctac agtcgcctgg tggaaacacc ttggcagagt	840
tgtttggtgc caggatgggc cactgaaggc atctgctgtg gacacacaca cacacacaca	900
cacacacaca cacacacaca gagagaggag agagaaagac acacgcacgc agagacacac	960
ggtcactgga attccattag aaaaaagtga gccgagcaag ggtagcggg agaagatttt	1020
tttgaatctt gtcttcgtct tgggtgcgaa gaagcgactc cagtctctcg tcctcgaagc	1080
tccgactgga ttgttcttgg gcgctgacac ccgtctgtgg atttcttttc tatttgcatt	1140
ttattccgac cccctccctc gccgcttct tccagccctt cactcgcaaa tcgcctctct	1200
ccccacctcc ccaggccct cctgggaagc gcaggggaat tggaccgcg gggactcacg	1260
ccttcccgga cgattggagg ggagggctga cccaggact gggctgttgg cttagaaagc	1320
cgatacacag atacgcgtat atttgattgt agcgggcaag gggggcgctg agaggcagca	1380
gcccacgccc cgctctcac cccacccct ccagccagag gcgagaatcg caggactcgg	1440
gatcttcac gggtggacta gctgggatct ccgcattgga tttggggctg attaccactg	1500
cttggctatt attattgttg ttgttactac tattattttt ttttaccxaa gggagaaaga	1560
caaaaaaacg gtgggattta tttaac atg atc ttg gca aac gtc ttc tgc ctc	1613
Met Ile Leu Ala Asn Val Phe Cys Leu	
1 5	
ttc ttc ttt cta gac gac acc ctc cgc tct ttg gcc agc cct tcc tcc	1661
Phe Phe Phe Leu Asp Asp Thr Leu Arg Ser Leu Ala Ser Pro Ser Ser	
10 15 20 25	
ctg cag ggc ccc gag ctc cac ggc tgg cgc ccc cca gtg gac tgt gtc	1709
Leu Gln Gly Pro Glu Leu His Gly Trp Arg Pro Pro Val Asp Cys Val	
30 35 40	
cgg gcc aat gag ctg tgt gcc gcc gaa tcc aac tgc agc tct cgc tac	1757
Arg Ala Asn Glu Leu Cys Ala Ala Glu Ser Asn Cys Ser Arg Tyr	
45 50 55	
cgc act ctg cgg cag tgc ctg gca ggc cgc gac cgc aac acc atg ctg	1805
Arg Thr Leu Arg Gln Cys Leu Ala Gly Arg Asp Arg Asn Thr Met Leu	
60 65 70	

gcc	aac	aag	gag	tgc	cag	gcg	gcc	ttg	gag	gtc	ttg	cag	gag	agc	ccg	1853
Ala	Asn	Lys	Glu	Cys	Gln	Ala	Ala	Leu	Glu	Val	Leu	Gln	Glu	Ser	Pro	
75						80					85					
ctg	tac	gac	tgc	cgc	tgc	aag	cgg	ggc	atg	aag	aag	gag	ctg	cag	tgt	1901
Leu	Tyr	Asp	Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu	Leu	Gln	Cys	
90					95					100					105	
ctg	cag	atc	tac	tgg	agc	atc	cac	ctg	ggg	ctg	acc	gag	ggt	gag	gag	1949
Leu	Gln	Ile	Tyr	Trp	Ser	Ile	His	Leu	Gly	Leu	Thr	Glu	Gly	Glu	Glu	
				110					115					120		
ttc	tac	gaa	gcc	tcc	ccc	tat	gag	ccg	gtg	acc	tcc	cgc	ctc	tcg	gac	1997
Phe	Tyr	Glu	Ala	Ser	Pro	Tyr	Glu	Pro	Val	Thr	Ser	Arg	Leu	Ser	Asp	
			125					130					135			
atc	ttc	agg	ctt	gct	tca	atc	ttc	tca	ggg	aca	ggg	gca	gac	ccg	gtg	2045
Ile	Phe	Arg	Leu	Ala	Ser	Ile	Phe	Ser	Gly	Thr	Gly	Ala	Asp	Pro	Val	
		140					145					150				
gtc	agc	gcc	aag	agc	aac	cat	tgc	ctg	gat	gct	gcc	aag	gcc	tgc	aac	2093
Val	Ser	Ala	Lys	Ser	Asn	His	Cys	Leu	Asp	Ala	Ala	Lys	Ala	Cys	Asn	
155						160					165					
ctg	aat	gac	aac	tgc	aag	aag	ctg	cgc	tcc	tcc	tac	atc	tcc	atc	tgc	2141
Leu	Asn	Asp	Asn	Cys	Lys	Lys	Leu	Arg	Ser	Ser	Tyr	Ile	Ser	Ile	Cys	
170					175					180					185	
aac	cgc	gag	atc	tcg	ccc	acc	gag	cgc	tgc	aac	cgc	cgc	aag	tgc	cac	2189
Asn	Arg	Glu	Ile	Ser	Pro	Thr	Glu	Arg	Cys	Asn	Arg	Arg	Lys	Cys	His	
				190					195					200		
aag	gcc	ctg	cgc	cag	ttc	ttc	gac	cgg	gtg	ccc	agc	gag	tac	acc	tac	2237
Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Arg	Val	Pro	Ser	Glu	Tyr	Thr	Tyr	
			205				210						215			
cgc	atg	ctc	ttc	tgc	tcc	tgc	caa	gac	cag	gcg	tgc	gct	gag	cgc	cgc	2285
Arg	Met	Leu	Phe	Cys	Ser	Cys	Gln	Asp	Gln	Ala	Cys	Ala	Glu	Arg	Arg	
		220					225					230				
cgg	caa	acc	atc	ctg	ccc	agc	tgc	tcc	tat	gag	gac	aag	gag	aag	ccc	2333
Arg	Gln	Thr	Ile	Leu	Pro	Ser	Cys	Ser	Tyr	Glu	Asp	Lys	Glu	Lys	Pro	
235						240					245					
aac	tgc	ctg	gac	ctg	cgt	ggc	gtg	tgc	cgg	act	gac	cac	ctg	tgt	cgg	2381
Asn	Cys	Leu	Asp	Leu	Arg	Gly	Val	Cys	Arg	Thr	Asp	His	Leu	Cys	Arg	
250					255					260					265	
tcc	cgg	ctg	gcc	gac	ttc	cat	gcc	aat	tgt	cga	gcc	tcc	tac	cag	acg	2429
Ser	Arg	Leu	Ala	Asp	Phe	His	Ala	Asn	Cys	Arg	Ala	Ser	Tyr	Gln	Thr	
				270					275					280		
gtc	acc	agc	tgc	cct	gcg	gac	aat	tac	cag	gcg	tgt	ctg	ggc	tct	tat	2477
Val	Thr	Ser	Cys	Pro	Ala	Asp	Asn	Tyr	Gln	Ala	Cys	Leu	Gly	Ser	Tyr	
			285					290					295			
gct	ggc	atg	att	ggg	ttt	gac	atg	aca	cct	aac	tat	gtg	gac	tcc	agc	2525
Ala	Gly	Met	Ile	Gly	Phe	Asp	Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser	Ser	
		300					305					310				
ccc	act	ggc	atc	gtg	gtg	tcc	ccc	tgg	tgc	agc	tgt	cgt	ggc	agc	ggg	2573
Pro	Thr	Gly	Ile	Val	Val	Ser	Pro	Trp	Cys	Ser	Cys	Arg	Gly	Ser	Gly	
	315					320					325					

aac atg gag gag gag tgt gag aag ttc ctc agg gac ttc acc gag aac Asn Met Glu Glu Glu Cys Glu Lys Phe Leu Arg Asp Phe Thr Glu Asn 330 335 340 345	2621
cca tgc ctc cgg aac gcc atc cag gcc ttt ggc aac ggc acg aac gtg Pro Cys Leu Arg Asn Ala Ile Gln Ala Phe Gly Asn Gly Thr Asn Val 350 355 360	2669
aac gtg tcc cca aaa ggc ccc tcg ttc cag gcc acc cag gcc cct cgg Asn Val Ser Pro Lys Gly Pro Ser Phe Gln Ala Thr Gln Ala Pro Arg 365 370 375	2717
gtg gag aag acg cct tct ttg cca gat gac ctc agt gac agt acc agc Val Glu Lys Thr Pro Ser Leu Pro Asp Asp Leu Ser Asp Ser Thr Ser 380 385 390	2765
ttg ggg acc agt gtc atc acc acc tgc acg tct gtc cag gag cag ggg Leu Gly Thr Ser Val Ile Thr Thr Cys Thr Ser Val Gln Glu Gln Gly 395 400 405	2813
ctg aag gcc aac aac tcc aaa gag tta agc atg tgc ttc aca gag ctc Leu Lys Ala Asn Asn Ser Lys Glu Leu Ser Met Cys Phe Thr Glu Leu 410 415 420 425	2861
acg aca aat atc atc cca ggg agt aac aag gtg atc aaa cct aac tca Thr Thr Asn Ile Ile Pro Gly Ser Asn Lys Val Ile Lys Pro Asn Ser 430 435 440	2909
ggc ccc agc aga gcc aga ccg tcg gct gcc ttg acc gtg ctg tct gtc Gly Pro Ser Arg Ala Arg Pro Ser Ala Ala Leu Thr Val Leu Ser Val 445 450 455	2957
ctg atg ctg aaa ctg gcc ttg taggctgtgg gaaccgagtc agaagatttt Leu Met Leu Lys Leu Ala Leu 460	3008
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aatgcccttc actttctcct ggtgtttttc tctctggacc cttctgaagc agagaccgga	3308
caagagcctg cagcgggaagg gactctgggc tgtgcctgag gctggctggg ggcaggacaa	3368
cacagctgct tccccaggct gccactctg gggaccgcgt gggggctggc agagggcatc	3428
ggtcagcggg gcagcggggc tggccatgag ggtccacctt cagccctttg gcttcaagga	3488
tggagatggg tttgccctcc ctctctgccc tcgggtgggg ctggtgggtc tgcagctggg	3548
gtgggaactt ccccacggat ggcgggtggag ggggttcgca ccgtgctggg ctccccctga	3608
ctgtagcacg gagtggtggg gctggggggc agctccagga gggcttgaga gctcagcctg	3668
cctgggagag cccttggtggc gaggcattaa aacttgggca ccagcttctt tctcgggtggc	3728
agaaattttg aagtcagaga gaaacgggcc tttgttggtc tctttgcttt ctcgtgggtc	3788
ctttggcagg cctccctttg gggagaggga ggggagagac cacagccggg tgtgtgtctg	3848

cagcacccgtg ggccctcaag ctttctgct gtcttctccc tctctctctt ttcccccttc 3908
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catatatgta tatacacatc catatacata tattgtgtgg tttccccctt ctttcctttt 4028
tttaagcaac aaaactatgg aaataatacc ccaacagatg agcgaaaatg tattattgta 4088
aagtttattt tttttaatac tggtgtctat aatggggaaa aaggacattg gccccgcagt 4148
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aaccaaggct ccaataaacg tgcg 4232

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<211> 464
<212> PRT
<213> HUMAN

<400> 36

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20 25 30

Gly Trp Arg Pro Pro Val Asp Cys Val Arg Ala Asn Glu Leu Cys Ala
35 40 45

Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu
50 55 60

Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala
65 70 75 80

Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys
85 90 95

Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile
100 105 110

His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro Tyr
115 120 125

Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile
130 135 140

Phe Ser Gly Thr Gly Ala Asp Pro Val Val Ser Ala Lys Ser Asn His
145 150 155 160

Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys
165 170 175

Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr
180 185 190

Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe
195 200 205

Asp Arg Val Pro Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser Cys
210 215 220

Gln Asp Gln Ala Cys Ala Glu Arg Arg Arg Gln Thr Ile Leu Pro Ser
225 230 235 240

Cys Ser Tyr Glu Asp Lys Glu Lys Pro Asn Cys Leu Asp Leu Arg Gly
245 250 255

Val Cys Arg Thr Asp His Leu Cys Arg Ser Arg Leu Ala Asp Phe His
260 265 270

Ala Asn Cys Arg Ala Ser Tyr Gln Thr Val Thr Ser Cys Pro Ala Asp
275 280 285

Asn Tyr Gln Ala Cys Leu Gly Ser Tyr Ala Gly Met Ile Gly Phe Asp
290 295 300

Met Thr Pro Asn Tyr Val Asp Ser Ser Pro Thr Gly Ile Val Val Ser
305 310 315 320

Pro Trp Cys Ser Cys Arg Gly Ser Gly Asn Met Glu Glu Glu Cys Glu
325 330 335

Lys Phe Leu Arg Asp Phe Thr Glu Asn Pro Cys Leu Arg Asn Ala Ile
340 345 350

Gln Ala Phe Gly Asn Gly Thr Asn Val Asn Val Ser Pro Lys Gly Pro
355 360 365

Ser Phe Gln Ala Thr Gln Ala Pro Arg Val Glu Lys Thr Pro Ser Leu
370 375 380

Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr Ser Val Ile Thr
385 390 395 400

Thr Cys Thr Ser Val Gln Glu Gln Gly Leu Lys Ala Asn Asn Ser Lys
405 410 415

Glu Leu Ser Met Cys Phe Thr Glu Leu Thr Thr Asn Ile Ile Pro Gly
420 425 430

Ser Asn Lys Val Ile Lys Pro Asn Ser Gly Pro Ser Arg Ala Arg Pro
435 440 445

Ser Ala Ala Leu Thr Val Leu Ser Val Leu Met Leu Lys Leu Ala Leu
450 455 460

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<211> 1991
<212> DNA
<213> HUMAN

<220>
<221> CDS
<222> (203)..(1402)

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agggcagtgaggaggtagt tttccatcct ccattccaggg gaggagcgag gggagcgagg 180
agcccgggcgc ctacagctcg cc atg gtg cgc ccc ctg aac ccg cga ccg ctg 232
Met Val Arg Pro Leu Asn Pro Arg Pro Leu
1 5 10
ccg ccc gta gtc ctg atg ttg ctg ctg ctg ctg ccg ccg tcg ccg ctg 280
Pro Pro Val Val Leu Met Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu
15 20 25
cct ctc gca gcc gga gac ccc ctt ccc aca gaa agc cga ctc atg aac 328
Pro Leu Ala Ala Gly Asp Pro Leu Pro Thr Glu Ser Arg Leu Met Asn
30 35 40
agc tgt ctc cag gcc agg agg aag tgc cag gct gat ccc acc tgc agt 376
Ser Cys Leu Gln Ala Arg Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser
45 50 55
gct gcc tac cac cac ctg gat tcc tgc acc tct agc ata agc acc cca 424
Ala Ala Tyr His His Leu Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro
60 65 70
ctg ccc tca gag gag cct tcg gtc cct gct gac tgc ctg gag gca gca 472
Leu Pro Ser Glu Glu Pro Ser Val Pro Ala Asp Cys Leu Glu Ala Ala
75 80 85 90
cag caa ctc agg aac agc tct ctg ata ggc tgc atg tgc cac cgg cgc 520
Gln Gln Leu Arg Asn Ser Ser Leu Ile Gly Cys Met Cys His Arg Arg
95 100 105
atg aag aac cag gtt gcc tgc ttg gac atc tat tgg acc gtt cac cgt 568
Met Lys Asn Gln Val Ala Cys Leu Asp Ile Tyr Trp Thr Val His Arg
110 115 120
gcc cgc agc ctt ggt aac tat gag ctg gat gtc tcc ccc tat gaa gac 616
Ala Arg Ser Leu Gly Asn Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp
125 130 135

aca	gtg	acc	agc	aaa	ccc	tgg	aaa	atg	aat	ctc	agc	aaa	ctg	aac	atg	664
Thr	Val	Thr	Ser	Lys	Pro	Trp	Lys	Met	Asn	Leu	Ser	Lys	Leu	Asn	Met	
	140					145					150					
ctc	aaa	cca	gac	tca	gac	ctc	tgc	ctc	aag	ttt	gcc	atg	ctg	tgt	act	712
Leu	Lys	Pro	Asp	Ser	Asp	Leu	Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	
	155				160					165					170	
ctc	aat	gac	aag	tgt	gac	cgg	ctg	cgc	aag	gcc	tac	ggg	gag	gcg	tgc	760
Leu	Asn	Asp	Lys	Cys	Asp	Arg	Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	
				175					180					185		
tcc	ggg	ccc	cac	tgc	cag	cgc	cac	gtc	tgc	ctc	agg	cag	ctg	ctc	act	808
Ser	Gly	Pro	His	Cys	Gln	Arg	His	Val	Cys	Leu	Arg	Gln	Leu	Leu	Thr	
			190					195					200			
ttc	ttc	gag	aag	gcc	gcc	gag	ccc	cac	gcg	cag	ggc	ctg	cta	ctg	tgc	856
Phe	Phe	Glu	Lys	Ala	Ala	Glu	Pro	His	Ala	Gln	Gly	Leu	Leu	Leu	Cys	
		205					210					215				
cca	tgt	gcc	ccc	aac	gac	cgg	ggc	tgc	ggg	gag	cgc	cgg	cgc	aac	acc	904
Pro	Cys	Ala	Pro	Asn	Asp	Arg	Gly	Cys	Gly	Glu	Arg	Arg	Arg	Asn	Thr	
	220					225					230					
atc	gcc	ccc	aac	tgc	gcg	ctg	ccg	cct	gtg	gcc	ccc	aac	tgc	ctg	gag	952
Ile	Ala	Pro	Asn	Cys	Ala	Leu	Pro	Pro	Val	Ala	Pro	Asn	Cys	Leu	Glu	
	235				240				245						250	
ctg	cgg	cgc	ctc	tgc	ttc	tcc	gac	ccg	ctt	tgc	aga	tca	cgc	ctg	gtg	1000
Leu	Arg	Arg	Leu	Cys	Phe	Ser	Asp	Pro	Leu	Cys	Arg	Ser	Arg	Leu	Val	
				255					260					265		
gat	ttc	cag	acc	cac	tgc	cat	ccc	atg	gac	atc	cta	gga	act	tgt	gca	1048
Asp	Phe	Gln	Thr	His	Cys	His	Pro	Met	Asp	Ile	Leu	Gly	Thr	Cys	Ala	
			270					275					280			
aca	gag	cag	tcc	aga	tgt	cta	cga	gca	tac	ctg	ggg	ctg	att	ggg	act	1096
Thr	Glu	Gln	Ser	Arg	Cys	Leu	Arg	Ala	Tyr	Leu	Gly	Leu	Ile	Gly	Thr	
		285					290					295				
gcc	atg	acc	ccc	aac	ttt	gcc	agc	aat	gtc	aac	acc	agt	gtt	gcc	tta	1144
Ala	Met	Thr	Pro	Asn	Phe	Ala	Ser	Asn	Val	Asn	Thr	Ser	Val	Ala	Leu	
	300					305					310					
agc	tgc	acc	tgc	cga	ggc	agt	ggc	aac	ctg	cag	gag	gag	tgt	gaa	atg	1192
Ser	Cys	Thr	Cys	Arg	Gly	Ser	Gly	Asn	Leu	Gln	Glu	Glu	Cys	Glu	Met	
	315				320					325					330	
ctg	gaa	ggg	ttc	ttc	tcc	cac	aac	ccc	tgc	ctc	acg	gag	gcc	att	gca	1240
Leu	Glu	Gly	Phe	Phe	Ser	His	Asn	Pro	Cys	Leu	Thr	Glu	Ala	Ile	Ala	
				335					340					345		
gct	aag	atg	cgt	ttt	cac	agc	caa	ctc	ttc	tcc	cag	gac	tgg	cca	cac	1288
Ala	Lys	Met	Arg	Phe	His	Ser	Gln	Leu	Phe	Ser	Gln	Asp	Trp	Pro	His	
			350					355					360			
cct	acc	ttt	gct	gtg	atg	gca	cac	cag	aat	gaa	aac	cct	gct	gtg	agg	1336
Pro	Thr	Phe	Ala	Val	Met	Ala	His	Gln	Asn	Glu	Asn	Pro	Ala	Val	Arg	
		365					370					375				
cca	cag	ccc	tgg	gtg	ccc	tct	ctt	ttc	tcc	tgc	acg	ctt	ccc	ttg	att	1384
Pro	Gln	Pro	Trp	Val	Pro	Ser	Leu	Phe	Ser	Cys	Thr	Leu	Pro	Leu	Ile	
	380					385					390					

ctg ctc ctg agc cta tgg tagctggact tccccagggc cctcttcccc 1432
 Leu Leu Leu Ser Leu Trp
 395 400

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 ggaggtgcag tgcgcagatg agggcacagg agaagctaag ggttatgacc tccagatcct 1552
 tactggtcca gtcctcattc cctccacccc atctccactt ctgattcatg ctgcccctcc 1612
 ttggtggcca caatttagcc atgtcatctg gtggtgacca gctccaccaa gcccttttgt 1672
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 cattccagat taggggttagg gtagggagga ctgggtgttc tgaggcagcc tagaaagtca 1792
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<210> 38
 <211> 400
 <212> PRT
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<400> 38

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Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
 20 25 30

Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
 35 40 45

Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Ala Ala Tyr His His Leu
 50 55 60

Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
 65 70 75 80

Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
 85 90 95

Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala
 100 105 110

Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn
 115 120 125

Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro
130 135 140

Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp
145 150 155 160

Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp
165 170 175

Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln
180 185 190

Arg His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala
195 200 205

Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp
210 215 220

Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala
225 230 235 240

Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe
245 250 255

Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys
260 265 270

His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys
275 280 285

Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe
290 295 300

Ala Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly
305 310 315 320

Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser
325 330 335

His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His
340 345 350

Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met
355 360 365

Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro
370 375 380

Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp
385 390 395 400

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<222> (684)..(2063)

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gagttaggct tgcttctggt tgtcttctaa aggcacgggtg atacagaatg atgagactag 180
gctggagggg gctttctgct tctctgtgtg tgaccttgag ttatctccct tcgttgatc 240
cgagctttcc tggaatatga tgttgaatat gaatatgagt tctgcctaag gtccagacag 300
gctctgaggg ttaactgact tttggagcct tcaaataaat accttggatg gagtgggggt 360
ttgtccaatg ggagttgagg caagatccct ttgcataagc cttgccacat catgttgaag 420
ccatgccatt ctgtctggac tattggcatc ttacctttcc agcagtttca gtgaaggcct 480
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gaaccatggt ttagggggag tatggccaac caggttgggt ctgtgttgac cttggctctg 600
gtgttctttt gtgtaaagtg ggtgagaagt tccttcaaac cttaggccta cattgggggtc 660
agagactgtg gtggccctca ttc atg ctt gtc ttc cct tcc cac tac cca gac 713
Met Leu Val Phe Pro Ser His Tyr Pro Asp
1 5 10
gaa acc ctc cgc tct ttg gcc agc cct tcc tcc ctg cag ggc tct gag 761
Glu Thr Leu Arg Ser Leu Ala Ser Pro Ser Ser Leu Gln Gly Ser Glu
15 20 25
ctc cac ggc tgg cgc ccc caa gtg gac tgt gtc cgg gcc aat gag ctg 809
Leu His Gly Trp Arg Pro Gln Val Asp Cys Val Arg Ala Asn Glu Leu
30 35 40
tgt gcg gct gaa tcc aac tgc agc tcc agg tac cgc acc ctt cgg cag 857
Cys Ala Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln
45 50 55
tgc ctg gca ggc cgg gat cgc aat acc atg ctg gcc aat aag gag tgc 905
Cys Leu Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys
60 65 70
cag gca gcc ctg gag gtc ttg cag gaa agc cca ctg tat gac tgc cgc 953
Gln Ala Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg
75 80 85 90

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Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu	Leu	Gln	Cys	Leu	Gln	Ile	Tyr	Trp	
			95						100					105		
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Ser	Ile	His	Leu	Gly	Leu	Thr	Glu	Gly	Glu	Glu	Phe	Tyr	Glu	Ala	Ser	
			110					115					120			
ccc	tat	gag	cct	gtg	acc	tcg	cgc	ctc	tcg	gac	atc	ttc	agg	ctc	gct	1097
Pro	Tyr	Glu	Pro	Val	Thr	Ser	Arg	Leu	Ser	Asp	Ile	Phe	Arg	Leu	Ala	
		125					130					135				
tca	atc	ttc	tca	ggg	aca	ggg	aca	gac	ccg	gcg	gtc	agt	acc	aaa	agc	1145
Ser	Ile	Phe	Ser	Gly	Thr	Gly	Thr	Asp	Pro	Ala	Val	Ser	Thr	Lys	Ser	
	140					145					150					
aac	cac	tgc	ctg	gat	gcc	gcc	aag	gcc	tgc	aac	ctg	aat	gac	aac	tgc	1193
Asn	His	Cys	Leu	Asp	Ala	Ala	Lys	Ala	Cys	Asn	Leu	Asn	Asp	Asn	Cys	
155					160					165					170	
aag	aag	ctt	cgc	tcc	tct	tat	atc	tcc	atc	tgc	aac	cgt	gag	atc	tct	1241
Lys	Lys	Leu	Arg	Ser	Ser	Tyr	Ile	Ser	Ile	Cys	Asn	Arg	Glu	Ile	Ser	
				175					180					185		
ccc	acc	gaa	cgc	tgc	aac	cgc	cgc	aag	tgc	cac	aag	gct	ctg	cgc	cag	1289
Pro	Thr	Glu	Arg	Cys	Asn	Arg	Arg	Lys	Cys	His	Lys	Ala	Leu	Arg	Gln	
			190					195					200			
ttc	ttt	gac	cgt	gtg	ccc	agc	gag	tat	acc	tac	cgc	atg	ctc	ttc	tgc	1337
Phe	Phe	Asp	Arg	Val	Pro	Ser	Glu	Tyr	Thr	Tyr	Arg	Met	Leu	Phe	Cys	
		205					210					215				
tcc	tgt	cag	gac	cag	gca	tgt	gct	gag	cgt	cgc	cgg	caa	acc	atc	ctg	1385
Ser	Cys	Gln	Asp	Gln	Ala	Cys	Ala	Glu	Arg	Arg	Arg	Gln	Thr	Ile	Leu	
	220					225					230					
ccc	agt	tgc	tcc	tat	gag	gac	aag	gag	aag	ccc	aac	tgc	ctg	gac	ctg	1433
Pro	Ser	Cys	Ser	Tyr	Glu	Asp	Lys	Glu	Lys	Pro	Asn	Cys	Leu	Asp	Leu	
235					240					245					250	
cgc	agc	ctg	tgt	cgt	aca	gac	cac	ctg	tgc	cgg	tcc	cga	ctg	gca	gat	1481
Arg	Ser	Leu	Cys	Arg	Thr	Asp	His	Leu	Cys	Arg	Ser	Arg	Leu	Ala	Asp	
				255					260					265		
ttc	cac	gcc	aac	tgt	cga	gcc	tcc	tac	cgg	aca	atc	acc	agc	tgt	cct	1529
Phe	His	Ala	Asn	Cys	Arg	Ala	Ser	Tyr	Arg	Thr	Ile	Thr	Ser	Cys	Pro	
			270					275					280			
gcg	gac	aac	tac	cag	gca	tgt	ctg	ggc	tcc	tat	gct	ggc	atg	att	ggg	1577
Ala	Asp	Asn	Tyr	Gln	Ala	Cys	Leu	Gly	Ser	Tyr	Ala	Gly	Met	Ile	Gly	
		285					290					295				
ttt	gat	atg	aca	ccc	aac	tat	gtg	gac	tcc	aac	ccc	acg	ggc	atc	gtg	1625
Phe	Asp	Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser	Asn	Pro	Thr	Gly	Ile	Val	
	300					305					310					
gtg	tct	ccc	tgg	tgc	aat	tgt	cgt	ggc	agt	ggg	aac	atg	gaa	gaa	gag	1673
Val	Ser	Pro	Trp	Cys	Asn	Cys	Arg	Gly	Ser	Gly	Asn	Met	Glu	Glu	Glu	
315					320					325					330	
tgt	gag	aag	ttc	ctc	agg	gac	ttc	acg	gaa	aac	cca	tgc	ctc	cgg	aat	1721
Cys	Glu	Lys	Phe	Leu	Arg	Asp	Phe	Thr	Glu	Asn	Pro	Cys	Leu	Arg	Asn	
				335					340					345		

gcc att cag gcc ttt ggt aat ggc aca gat gtg aac atg tct ccc aaa 1769
Ala Ile Gln Ala Phe Gly Asn Gly Thr Asp Val Asn Met Ser Pro Lys
350 355 360

ggc ccc tca ctc cca gct acc cag gcc cct cgg gtg gag aag act cct 1817
Gly Pro Ser Leu Pro Ala Thr Gln Ala Pro Arg Val Glu Lys Thr Pro
365 370 375

tca ctg cca gat gac ctc agt gac agc acc agc ctg ggg acc agt gtc 1865
Ser Leu Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr Ser Val
380 385 390

atc acc acc tgc aca tct atc cag gag caa ggg ctg aag gcc aac aac 1913
Ile Thr Thr Cys Thr Ser Ile Gln Glu Gln Gly Leu Lys Ala Asn Asn
395 400 405 410

tcc aaa gag tta agc atg tgc ttc aca gag ctc acg aca aac atc agt 1961
Ser Lys Glu Leu Ser Met Cys Phe Thr Glu Leu Thr Thr Asn Ile Ser
415 420 425

cca ggg agt aaa aag gtg atc aaa ctt aac tca ggc tcc agc aga gcc 2009
Pro Gly Ser Lys Lys Val Ile Lys Leu Asn Ser Gly Ser Ser Arg Ala
430 435 440

aga ctg tcg gct gcc ttg act gcc ctc cca ctc ctg atg ctg acc ttg 2057
Arg Leu Ser Ala Ala Leu Thr Ala Leu Pro Leu Leu Met Leu Thr Leu
445 450 455

gcc ttg taggcctttg gaaccagca caaaagtct tcaagcaacc cagatatgaa 2113
Ala Leu
460

ctcccgctg acaaaatgga aacacacgca tacacacatg ccacacacag acacacacac 2173

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Ser	Arg 130	Leu	Ser	Asp	Ile	Phe 135	Arg	Leu	Ala	Ser	Ile 140	Phe	Ser	Gly	Thr
Gly 145	Thr	Asp	Pro	Ala	Val 150	Ser	Thr	Lys	Ser	Asn 155	His	Cys	Leu	Asp	Ala 160
Ala	Lys	Ala	Cys	Asn 165	Leu	Asn	Asp	Asn	Cys 170	Lys	Lys	Leu	Arg	Ser 175	Ser
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Ser	Glu 210	Tyr	Thr	Tyr	Arg	Met 215	Leu	Phe	Cys	Ser	Cys 220	Gln	Asp	Gln	Ala
Cys 225	Ala	Glu	Arg	Arg	Arg 230	Gln	Thr	Ile	Leu	Pro 235	Ser	Cys	Ser	Tyr	Glu 240
Asp	Lys	Glu	Lys	Pro 245	Asn	Cys	Leu	Asp	Leu 250	Arg	Ser	Leu	Cys	Arg 255	Thr
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Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp	Arg	
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Pro	Met	Asp	Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys	Leu	
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aggcaggagg aacacagaaca gacaagcatt gtcttttgtc attgctcgaa gtgcaagcgt 3060
gcatacctgt ggaggggaact ggtggctgct tgtaaagtgt ctgcagcatc tcttgacaca 3120
cttgtcatga cacaatccag taccttggtt ttcaggttat ctgacaaagg cagctttgat 3180
tgggacatgg aggcattggc aggccggaa 3209

<210> 46
<211> 508
<212> DNA
<213> HUMAN

<400> 46
tctggcctcg gaacacgcca ttctccgccc cgcttccaat aaccactaac atccctaacg 60
agcatccgag ccgagggtc tgctcgga aaatcctggc ccaactcggc ccttcgagct 120
ctcgaagatt accgcatcta tttttttttt cttttttttt ttttcctagc gcagataaag 180
tgagcccgga aaggggaagga gggggcgggg acaccattgc cctgaaagaa taaataagta 240
aataa caaaa ctggctcctc gccgcagctg gacgcggctc gttgagtcca ggttgggtcg 300
gacctgaacc cctaaaagcg gaaccgcctc ccgccctcgc catcccgag ctgagtcgcc 360
ggcgggcgtg gctgctgcca gaccggaggt ttctcttttc actggatgga gctgaacttt 420
ggcgggccag agcagcacag ctgtccgggg atcgtgcac gctgagctcc ctcggaaga 480
cccagcggcg gctcgggatt tttttggg 508

<210> 47
<211> 510
<212> DNA
<213> HUMAN

<400> 47
aatctggcct cggaacacgc cattctccgc gccgcttcca ataaccacta acatccctaa 60
cgagcatccg agccgagggc tctgctcgga aatcgtcctg gcccaactcg gcccttcgag 120
ctctcgaaga ttaccgcac tttttttttt ttcttttttt tcttttctta gcgcagataa 180
agtgagcccg gaaaggggaag gagggggcgg ggacaccatt gccctgaaag aataaataag 240

taaataaaca aactggctcc tcgccgcagc tggacgcggt cggttgagtc caggttgggt 300
cggacctgaa cccctaaaag cggaaccgcc tcccgccctc gccatcccgg agctgagtcg 360
ccggcggcgg tggtctgctgc cagaccggga gtttcctctt tcaactggatg gagctgaact 420
ttgggcggcc agagcagcac agctgtccgg ggatcgctgc acgctgagct ccctcggcaa 480
gaccagcgg cggtctggga tttttttggg 510

<210> 48
<211> 1927
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (550)..(550)
<223> N in position 550 indicates any nucleic acid

<400> 48
tctggcctcg gaacacgcca ttctccgcgc cgcttccaat aaccactaac atccctaacg 60
agcatccgag ccgagggctc tgctcggaaa tcgtcctggc ccaactcggc ccttcgagct 120
ctcgaagatt accgcatcta tttttttttt cttttttttt ttttcctagc gcagataaag 180
tgagcccgga aagggaagga gggggcgggg acaccattgc cctgaaagaa taaataagta 240
aataaaciaa ctggctcctc gccgcagctg gacgcggtcg gttgagtcca ggttgggtcg 300
gacctgaacc cctaaaagcg gaaccgcctc ccgccctcgc catcccggag ctgagtcgcc 360
ggcggcgggtg gctgctgcca gaccgggagt ttctcttttc actggatgga gctgaacttt 420
gggcggccag agcagcacag ctgtccgggg atcgctgcac gctgagctcc ctccggcaaga 480
cccagcggcg gctcgggatt tttttggggg ggccggggacc agccccgcgc cggcaccatg 540
ttcctggcgn ccctgtactt cgcgctgccg ctcttggact tgctcctgtc ggccgaagtg 600
agcggcggag accgcctgga ttgcgtgaaa gccagtgatc agtgccctgaa ggagcagagc 660
tgagcacca agtaccgcac gctaaggcag tgctgggcgg gcaaggagac caacttcagc 720
ctggcatccg gcctggaggc caaggatgag tgccgcagcg ccatggaggc cctgaagcag 780
aagtcgctct acaactgccg ctgcaagcgg ggtatgaaga aggagaagaa ctgcctgcgc 840
atttactgga gcatgtacca gagcctgcag ggaaatgatc tgctggagga ttccccatat 900
gaaccagtta acagcagatt gtcagatata ttccgggtgg tccattcat atcagatgtt 960
tttcagcaag tggagcacat tcccaaaggg aacaactgcc tggatgcagc gaaggcctgc 1020
aacctcgacg acatttgcaa gaagtacagg tcggcgtaca tcaccccgctg caccaccagc 1080
gtgtccaacg atgtctgcaa ccgccgcaag tgccacaagg ccctccggca gttctttgac 1140
aagggtcccgg ccaagcacag ctacggaatg ctcttctgct cctgccggga catgcctgc 1200

acagagcgga	ggcgacagac	catcgtgcct	gtgtgctcct	atgaagagag	ggagaagccc	1260
aactgtttga	atttgcagga	ctcctgcaag	acgaattaca	tctgcagatc	tcgccttgcg	1320
gattttttta	ccaactgcc	gccagagtca	aggtctgtca	gcagctgtct	aaaggaaaac	1380
tacgtgact	gcctcctcgc	ctactcgggg	cttattggca	cagtcatgac	ccccaactac	1440
atagactcca	gtagcctcag	tgtggcccca	tgggtgtgact	gcagcaacag	tgggaacgac	1500
ctagaagagt	gcttgaaatt	tttgaatttc	ttcaaggaca	atacatgtct	taaaaatgca	1560
attcaagcct	ttggcaatgg	ctccgatgtg	accgtgtggc	agccagcctt	cccagtacag	1620
accaccactg	ccactaccac	cactgccctc	cgggttaaga	acaagcccct	ggggccagca	1680
gggtctgaga	atgaaattcc	cactcatgtt	ttgccaccgt	gtgcaaattt	acaggcacag	1740
aagctgaaat	ccaatgtgtc	gggcaataca	cacctctgta	tttccaatgg	taattatgaa	1800
aaagaaggtc	tcggtgcttc	cagccacata	accacaaaat	caatggctgc	tcctccaagc	1860
tgtggtctga	gcccactgct	ggtcctgggtg	gtaaccgctc	tgtccaccct	attatcttta	1920
acagaaa						1927

<210> 49
<211> 1929
<212> DNA
<213> HUMAN

<400> 49	
aatctggcct	cggaacacgc cattctccgc gccgcttcca ataaccacta acatccctaa 60
cgagcatccg	agccgagggc tctgctcgga aatcgtcctg gcccaactcg gcccttcgag 120
ctctcgaaga	ttaccgcac tatttttttt ttcttttttt tcttttccta gcgcagataa 180
agtgagcccg	gaaaggggaag gagggggcgg ggacaccatt gccctgaaag aataaataag 240
taaataaaca	aactggctcc tcgccgcagc tggacgcggt cggttgagtc cagggtgggt 300
cggacctgaa	cccctaaaag cggaaccgcc tcccgcctc gccatcccgg agctgagtcg 360
ccggcggcgg	tggctgctgc cagacccgga gtttcctctt tctactggatg gagctgaact 420
ttgggcggcc	agagcagcac agctgtccgg ggatcgctgc acgctgagct ccctcggcaa 480
gaccagcgg	cggctcggga tttttttggg ggggcgggga ccagccccgc gccggcacca 540
tgttcctggc	gacctgtac ttccgcgtgc cgctcttggc cttgctcctg tcggccgaag 600
tgagcggcgg	agaccgcctg gattgcgtga aagccagtga tcagtgcctg aaggagcaga 660
gctgcagcac	caagtaccgc acgctaaggc agtgcgtggc gggcaaggag accaacttca 720
gcctggcatc	cggcctggag gccaaaggatg agtgccgcag cgccatggag gccctgaagc 780
agaagtcgct	ctacaactgc cgctgcaagc ggggtatgaa gaaggagaag aactgcctgc 840
gcatttactg	gagcatgtac cagagcctgc agggaaatga tctgctggag gattccccat 900
atgaaccagt	taacagcaga ttgtcagata tattccgggt ggtcccatc atatcagatg 960

tttttcagca agtgggagcac attcccaaag ggaacaactg cctggatgca gcgaaggcct 1020
gcaacctcga cgacatttgc aagaagtaca ggtcggcgta catcaccccg tgcaccacca 1080
gcgtgtccaa cgatgtctgc aaccgccgca agtgccacaa ggccctccgg cagttctttg 1140
acaaggtccc ggccaagcac agctacggaa tgctcttctg ctctgcccgg gacatcgct 1200
gcacagagcg gaggcgacag accatcgtgc ctgtgtgctc ctatgaagag agggagaagc 1260
ccaactgttt gaatttgcag gactcctgca agacgaatta catctgcaga tctcgcttg 1320
cggatttttt taccaactgc cagccagagt caagggtctgt cagcagctgt ctaaaggaaa 1380
actacgctga ctgcctctc gcctactcgg ggcttattgg cacagtcatg acccccaact 1440
acatagactc cagtagcctc agtgtggccc catggtgtga ctgcagcaac agtgggaacg 1500
acctagaaga gtgcttgaaa tttttgaatt tcttcaagga caatacatgt cttaaaaatg 1560
caattcaagc ctttggcaat ggctccgatg tgaccgtgtg gcagccagcc tcccagtac 1620
agaccaccac tgccactacc accactgccc tccgggttaa gaacaagccc ctggggccag 1680
caggggtctga gaatgaaatt cccactcatg ttttgccacc gtgtgcaaatt ttacaggcac 1740
agaagctgaa atccaatgtg tcgggcaata cacacctctg tatttccaat ggtaattatg 1800
aaaaagaaggt tctcggtgct tccagccaca taaccacaaa atcaatggct gctcctccaa 1860
gctgtggtct gagcccactg ctggctctgg tggttaaccgc tctgtccacc ctattatctt 1920
taacagaaa 1929

<210> 50
<211> 699
<212> DNA
<213> HUMAN

<400> 50
gtcggcgctac atcaccccggt gcaccaccag cgtgtccaat gatgtctgca accgccgcaa 60
gtgccacaag gccctccggc agttctttga caagggtccc gccaagcaca gctacggaat 120
gctctttctgc tcctgccggg acatcgcttg cacagagcgg aggcgacaga ccatcgtgcc 180
tgtgtgctcc tatgaagaga gggagaagcc caactgtttg aatttgcagg actcctgcaa 240
gacgaattac atctgcagat ctgccttgc ggattttttt accaactgcc agccagagtc 300
aagggtctgtc agcagctgtc taaaggaaaa ctacgtgac tgcctcctcg cctactcggg 360
gcttatttggc acagtcatga ccccaacta catagactcc agtagcctca gtgtggcccc 420
atgggtgtgac tgcagcaaca gtgggaacga cctagaagag tgcttgaaat ttttgaattt 480
cttcaaggac aatacatgtc ttaaaaatgc aattcaagcc tttggcaatg gctccgatgt 540
gaccgtgtgg cagccagcct tcccagtaca gaccaccact gccgtacca ccactgcctt 600
ccgggttaag aacaagcccc tggggccagc aggggtctgag aatgaaattc ccactcatgt 660

tttgccaccg tgtgcaaatt tacaggcaca gaagctgaa

699

<210> 51
<211> 2158
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1027)..(1027)
<223> N in position 1027 indicates a position of divergence between different receptor clones.

<220>
<221> misc_feature
<222> (1205)..(1243)
<223> N in positions 1205 to 1243 indicates positions of divergence between different receptor clones.

<400> 51
gtcggcgtag atcaccccggt gcaccaccag cgtgtccaat gatgtctgca accgccgcaa 60
gtgccacaag gccctccggc agttctttga caaggtcccg gccaagcaca gctacggaat 120
gctcttctgc tcctgccggg acatcgccctg cacagagcgg aggcgacaga ccatcgtgcc 180
tgtgtgctcc tatgaagaga gggagaagcc caactgtttg aatttgcagg actcctgcaa 240
gacgaattac atctgcagat ctgccttgc ggattttttt accaactgcc agccagagtc 300
aaggtctgtc agcagctgtc taaaggaaaa ctacgtgtac tgctctctcg cctactcggg 360
gcttattggc acagtcatga cccccaacta catagactcc agtagcctca gtgtggcccc 420
atggtgtgac tgcagcaaca gtgggaacga cctagaagag tgcttgaaat ttttgaattt 480
cttcaaggac aatacatgtc ttaaaaatgc aattcaagcc tttggcaatg gctccgatgt 540
gaccgtgtgg cagccagcct tcccagtaca gaccaccact gccgctacca ccaactgcct 600
ccgggttaag aacaagcccc tggggccagc aggggtctgag aatgaaattc ccaactcatgt 660
tttgccaccg tgtgcaaatt tacaggcaca gaagctgaaa tccaatgtgt cgggcaatac 720
acacctctgt atttccaatg gtaattatga aaaagaaggt ctcggtgctt ccagccacat 780
aaccacaaaa tcaatggctg ctcttccaag ctgtggtctg agcccactgc tggctcctggt 840
ggtaaccgct ctgtccacc tatttatcttt aacagaaaca tcatagctgc attaaaaaaa 900
tacaatatgg acatgtaaaa agacaaaaac caagttatct gtttctgtt ctcttgata 960
gctgaaattc cagtttagga gctcagttga gaaacagttc cattcaactg gaacattttt 1020
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cagtgtcca tccaaactca gaaggctttg ggatatgctg tatttttaaag ggacagtttg 1140
taacttgggc tgtaaagcaa actggggctg tgttttcgat gatgatgatc atcatgatca 1200
tgatnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnngatttta acagttttac 1260

ttctggcctt tcctagctag agaaggagtt aatatttcta aggtaactcc catatctcct 1320
ttaatgacat tgattttctaa tgatataaat ttcagcctac attgatgcc a gctttttttg 1380
ccacaaagaa gattcttacc aagagtgggc tttgtggaaa cagctggtac tgatgttcac 1440
ctttatatat gtactagcat tttccacgct gatgtttatg tactgtaaac agttctgcac 1500
tcttgtacaa aagaaaaaac acctgtcaca tccaaatata gtatctgtct tttcgtcaaa 1560
atagagagtg gggaatgagt gtgccgattc aatacctcaa tccctgaacg acactctcct 1620
aatcctaagc cttacctgag tgagaagccc tttacctaac aaaagtccaa tatagctgaa 1680
atgtcgctct aatactcttt acacatatga ggttatatgt agaaaaaaat tttactacta 1740
aatgatttca actattggct ttctatatatt tgaaagtaat gatattgtct cattttttta 1800
ctgatggttt aatacaaaaat acacagagct tgtttccctc cataagtagt gttecgctctg 1860
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agaaagtctt gcatcatgtg actgtggaca ggcaggagga aacagaacag acaagcattg 1980
tcttttgtca ttgctcgaag tgcaagcgtg catacctgtg gagggaaactg gtggctgctt 2040
gtaaagtctt tgcagcatct cttgacacac ttgtcatgac acaatccagt accttggttt 2100
tcaggttatc tgacaaaggc agctttgatt gggacatgga ggcatgggca ggccggaa 2158

<210> 52
<211> 659
<212> DNA
<213> HUMAN

<400> 52
gaatttgcag gactcctgca agacgaatta catctgcaga tctcgccttg cggatttttt 60
taccaactgc cagccagagt caaggtctgt cagcagctgt ctaaaggaaa actacgctga 120
ctgcctcctc gcctactcgg ggcttatttg cacagtcatg accccaact acatagactc 180
cagtagcctc agtgtggccc catggtgtga ctgcagcaac agtgggaacg acctagaaga 240
gtgcttgaaa tttttgaatt tcttcaagga caatacatgt cttaaaaatg caattcaagc 300
ctttggcaat ggctccgatg tgaccgtgtg gcagccagcc ttcccagtac agaccaccac 360
tgccactacc accactgccc tccgggttaa gaacaagccc ctggggccag cagggctctga 420
gaatgaaatt cccactcatg ttttgccacc gtgtgcaa at ttacaggcac agaagctgaa 480
atccaatgtg tcgggcaata cacacctctg tatttccaat ggtaattatg aaaaagaagg 540
tctcgggtgct tccagccaca taaccacaaa atcaatggct gctcctccaa gctgtggtct 600
gagcccactg ctggctcctg tggttaaccgc tctgtccacc ctattatctt taacagaaa 659

<210> 53
<211> 630
<212> DNA
<213> HUMAN

<400> 53
acatctgcag atctcgcctt gcggattttt ttaccaactg ccagccagag tcaaggctctg 60
tcagcagctg tctaaaggaa aactacgctg actgcctcct cgcctactcg gggcttattg 120
gcacagtcac gacccccaac tacatagact ccagtagcct cagtgtggcc ccatgggtgtg 180
actgcagcaa cagtgggaac gacctagaag agtgcttgaa atttttgaat ttcttcaagg 240
acaatacatg tcttaaaaaat gcaattcaag cttttggcaa tggctccgat gtgaccgtgt 300
ggcagccagc cttcccagta cagaccacca ctgccactac caccactgcc ctccgggtta 360
agaacaagcc cctggggcca gcagggtctg agaatgaaat tccactcat gttttgccac 420
cgtgtgcaaa ttacaggca cagaagctga aatccaatgt gtcgggcaat acacacctct 480
gtatttccaa tggtattat gaaaaagaag gtctcgggtgc ttccagccac ataaccacaa 540
aatcaatggc tgctcctcca agctgtggtc tgagcccact gctggctctg gtggttaaccg 600
ctctgtccac cctattatct ttaacagaaa 630

<210> 54
<211> 1076
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (586)..(586)
<223> N in position 586 indicates a position of divergence between different receptor clones.

<220>
<221> misc_feature
<222> (764)..(802)
<223> N in positions 764 to 802 indicates positions of divergence between different receptor clones.

<400> 54
tggaacgac ctagaagagt gcttgaaatt tttgaatttc ttcaaggaca atacatgtct 60
taaaaatgca attcaagcct ttggcaatgg ctccgatgtg accgtgtggc agccagcctt 120
cccagtacag accaccactg ccactaccac cactgccctc cgggttaaga acaagcccct 180
ggggccagca gggctctgaga atgaaattcc cactcatgtt ttgccaccgt gtgcaaattt 240
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taattatgaa aaagaaggct tcgggtgcttc cagccacata accacaaaat caatggctgc 360
tcctccaagc tgtggtctga gccactgct ggtcctgggtg gtaaccgctc tgtccaccct 420
attatcttta acagaaacat catagctgca ttaaaaaaat acaatatgga catgtaaaaa 480
gacaaaaacc aagttatctg tttcctgttc tcttgatatag ctgaaattcc agtttaggag 540
ctcagttgag aaacagttcc attcaactgg aacatTTTTT tttttncctt ttaagaaagc 600

ttcttgtgat ccttcggggc ttctgtgaaa aacctgatgc agtgctccat ccaaactcag 660
aaggcttttg gatatgctgt attttaaagg gacagtttgt aacttgggct gtaaagcaaa 720
ctggggctgt gttttcgaat atgatgatca tcatgatcat gatnnnnnnnn nnnnnnnnnn 780
nnnnnnnnnn nnnnnnnnnn nngattttta cagttttact tctggccttt cctagctaga 840
gaaggagtta atattttctaa ggtaactccc atatctcctt taatgacatt gattttctaatt 900
gatataaatt tcagcctaca ttgatgccaa gcttttttgc cacaagaag attcttacca 960
agagtgggct ttgtggaaac agctggtact gatgttcacc tttatatatg tactagcatt 1020
ttccacgctg atgtttatgt actgtaaaca gttctgcact cttgtacaaa agaaaa 1076

<210> 55
<211> 1059
<212> DNA
<213> HUMAN

<400> 55
agtgttgaa atttttgaat ttcttcaagg acaatacatg tcttaaaaat gcaattcaag 60
cctttggcaa tggctccgat gtgaccgtgt ggcagccagc cttcccagta cagaccacca 120
ctgccactac caccactgcc ctccgggtta agaacaagcc cctggggcca gcagggtctg 180
agaatgaaat tcccactcat gttttgccac cgtgtgcaaa tttacaggca cagaagctga 240
aatccaatgt gtcgggcaat acacacctct gtattttcaa tggtaattat gaaaaagaag 300
gtctcgggtgc ttccagccac ataaccacaa aatcaatggc tgctcctcca agctgtgggtc 360
tgagcccact gctggctctg gtggttaaccg ctctgtccac cctattatct ttaacagaaa 420
catcatagct gcattaaaaa aatacaatat ggacatgtaa aaagacaaaa accaagttat 480
ctgtttcctg ttctcttgta tagctgaaat tccagtttag gagctcagtt gagaaacagt 540
tccattcaac tggaacattt ttttttttct cttttaagaa agcttcttgt gatccttttg 600
ggcttctgtg aaaaacctga tgcagtgtct catccaaact cagaaggctt tgggatatgc 660
tgtattttta agggacagtt tgtaacttgg gctgtaaagc aaactggggc tgtgttttcg 720
atgatgatga tgatcatgat gatgatcatc atgatcatga tgatgatcat catgatcatg 780
atgatgattt taacagtttt acttctggcc tttcctagct agagaaggag ttaatatctc 840
taaggtaact cccatatctc ctttaatgac attgatttct aatgatataa atttcagcct 900
acattgatgc caagcttttt tgccacaaag aagattctta ccaagagtgg gctttgtgga 960
aacagctgggt actgatgttc acctttatat atgtactagc attttccacg ctgatgttta 1020
tgtactgtaa acagttctgc actcttgtac aaaagaaaa 1059

<210> 56
<211> 468
<212> PRT
<213> Mus musculus

<400> 56

Met	Phe	Leu	Ala	Thr	Leu	Tyr	Phe	Val	Leu	Pro	Leu	Leu	Asp	Leu	Leu	1	5	10	15
Met	Ser	Ala	Glu	Val	Ser	Gly	Gly	Asp	Arg	Leu	Asp	Cys	Val	Lys	Ala	20	25	30	
Ser	Asp	Gln	Cys	Leu	Lys	Glu	Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	Thr	35	40	45	
Leu	Arg	Gln	Cys	Val	Ala	Gly	Lys	Glu	Thr	Asn	Phe	Ser	Leu	Thr	Ser	50	55	60	
Gly	Leu	Glu	Ala	Lys	Asp	Glu	Cys	Arg	Ser	Ala	Met	Glu	Ala	Leu	Lys	65	70	75	80
Gln	Lys	Ser	Leu	Tyr	Asn	Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu	85	90	95	
Lys	Asn	Cys	Leu	Arg	Ile	Tyr	Trp	Ser	Met	Tyr	Gln	Ser	Leu	Gln	Gly	100	105	110	
Asn	Asp	Leu	Leu	Glu	Asp	Ser	Pro	Tyr	Glu	Pro	Val	Asn	Ser	Arg	Leu	115	120	125	
Ser	Asp	Ile	Phe	Arg	Ala	Val	Pro	Phe	Ile	Ser	Asp	Val	Phe	Gln	Gln	130	135	140	
Val	Glu	His	Ile	Ser	Lys	Gly	Asn	Asn	Cys	Leu	Asp	Ala	Ala	Lys	Ala	145	150	155	160
Cys	Asn	Leu	Asp	Asp	Thr	Cys	Lys	Lys	Tyr	Arg	Ser	Ala	Tyr	Ile	Thr	165	170	175	
Pro	Cys	Thr	Thr	Ser	Met	Ser	Asn	Glu	Val	Cys	Asn	Arg	Arg	Lys	Cys	180	185	190	
His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser	195	200	205	
Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	Val	Ala	Cys	Thr	Glu	Arg	210	215	220	
Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Arg	225	230	235	240

Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
245 250 255

Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
260 265 270

Ser Val Ser Asn Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
275 280 285

Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Val Asp Ser
290 295 300

Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
305 310 315 320

Asp Leu Glu Asp Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
325 330 335

Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
340 345 350

Met Trp Gln Pro Ala Pro Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
355 360 365

Thr Ala Phe Arg Ile Lys Asn Lys Pro Ser Gly Pro Ala Cys Ser Glu
370 375 380

Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
385 390 395 400

Gln Lys Leu Lys Ser Asn Val Ser Gly Ser Thr His Leu Cys Leu Ser
405 410 415

Asp Asn Asp Tyr Gly Lys Asp Gly Leu Ala Gly Ala Ser Ser His Ile
420 425 430

Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Ser Leu
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Pro Val Met Val Phe Thr Ala Leu Ala Ala Leu Leu Ser Val Ser Leu
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Ala Glu Thr Ser
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